

84692

Access DB# _____

SEARCH REQUEST FORM

CRFE

Scientific and Technical Information Center

Requester's Full Name: Torin Examiner #: 69507 Date: _____
 Art Unit: 1646 Phone Number 30 8-6208 Serial Number: 09/942374
 Mail Box and Bldg/Room Location: 91 Results Format Preferred (circle): PAPER DISK E-MAIL
10015

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

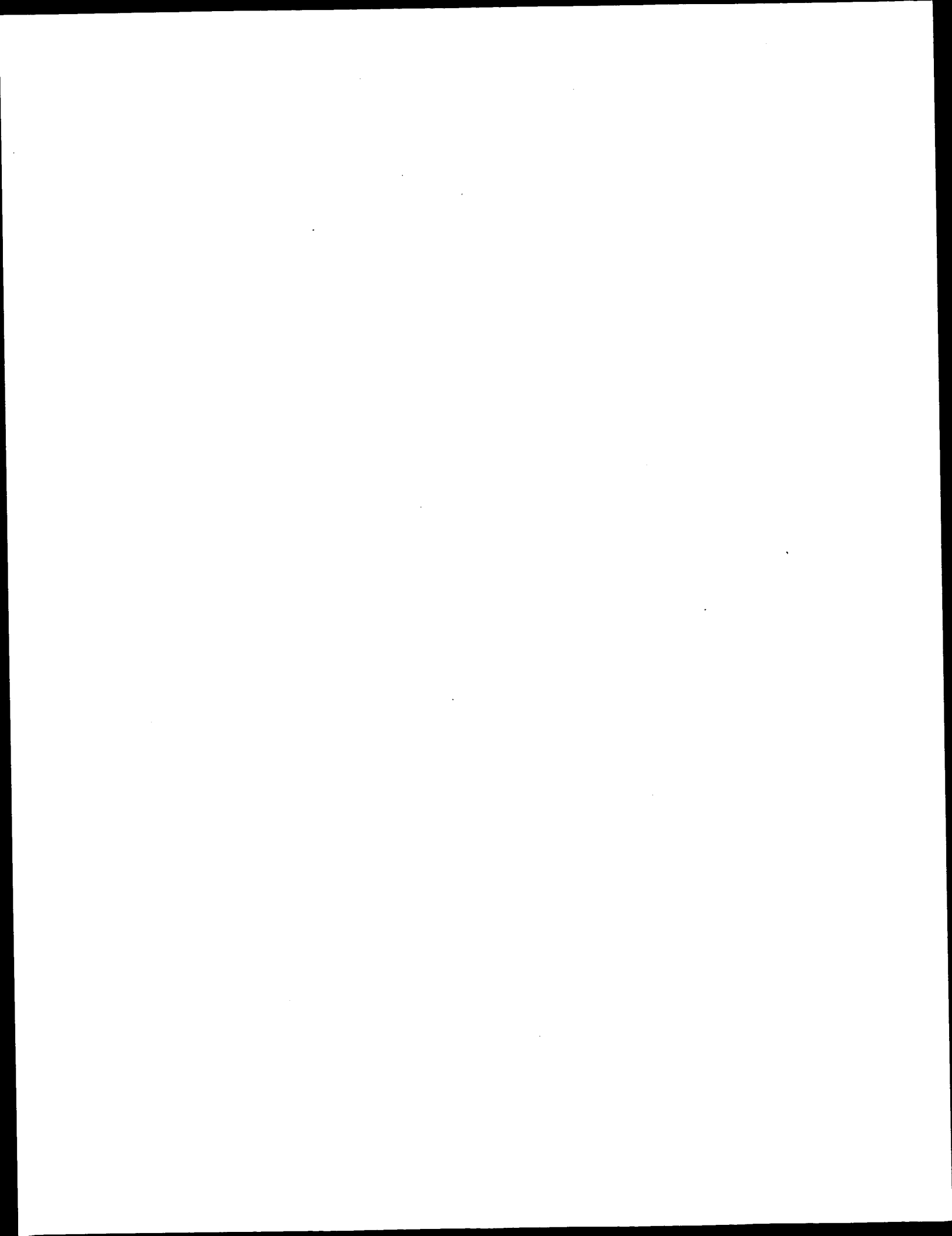
Please search SEQ ID NO: 1 and 2
 of 09/942374.

Point of Contact:
 Beverly Shears
 Technical Info. Specialist
 CM1 1E05 Tel: 308-4994

1-1194 NA
 2-346 AA

STAFF USE ONLY

Type of Search		Vendors and cost where applicable
Searcher: <u>Beverly e4094</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: <u>04-04-03</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>5</u>	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>20</u>	Other _____	Other (specify) <u>VCGN</u>



GenCore version 5.1.3
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Run on: April 3, 2003, 20:24:11 ; Search time 3676 Seconds

(without alignments)
9452.870 Million cell updates/sec

Title: US-09-942-374-1
Page: 1104

Sequence: 1 gcaccagccaaccacacac.....acattgttgatgycactga 1194

Scoring table: IDENTITY_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum	DB	seq	length:	0
Maximum	DB	seq	length:	20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database

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 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
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 32: em_hhg_other:*
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 39: em_hhg_hum:*
 40: em_hhg_mus:*
 41: em_hhg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

C	Result No.	Score	Query		DB	ID	Description
			Match	Length			
c	1	1193.6	100.0	1194	6	AX395166	AX395169 Sequence
	2	1187.2	99.4	1441	6	AB065866	AB065866 Homo sapi
	3	1187.2	99.4	1730	6	AX377635	AX377635 Sequence
	4	1187.2	99.4	2331	6	AX329907	AX329907 Sequence
	5	1187.2	99.4	2345	9	AF385432	AF385432 Homo sapi
	6	1187.2	99.4	3512	9	AF385431	AF385431 Homo sapi
	7	1187.2	99.4	179703	2	AC026631	AC026631 Homo sapi
	8	1187.2	99.4	210805	2	AC026633	AC026633 Homo sapi
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	10	1079.8	90.4	1083	6	AX305131	AX305131 Sequence
	11	1044.8	87.5	1050	6	AX338371	AX338371 Sequence
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	13	1041	87.2	1041	6	AX395171	AX395171 Sequence
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	21	374.3	31.3	1174	6	AX384661	AX384661 Sequence
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	25	369.2	30.9	1564	9	AB065885	AB065885 Homo sapi
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	42	190.4	15.9	1594	6	E31720	E31720 cDNA clone
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	44	190.4	15.9	157758	6	AC098824	AC098824 Homo sapi
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ALIGNMENTS

RESULT 1				
AX395169				
LOCUS	AX395169	1194 bp	DNA	linear
DEFINITION	Sequence 1 from Patent WO0218579.			PAT 18-MAY-2002
ACCESSION	AX395169			
VERSION	AX395169.1	GI:21066219		
KEYWORDS	.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1			
AUTHORS	Gluckemann, M.A.			
TITLE	57242, a novel human g protein-coupled receptor family member and uses therefor			

JOURNAL Patent: WO 0218579-A 1 07-MAR-2002;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers

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/organism="Homo sapiens"
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ORIGIN

Query Match 100.0%; Score 1193.6; DB 6; Length 1194;
Best Local Similarity 100.0%; Pred. No. 2.9e-287;
Matches 1194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCACGACGACCAACCAACACACAGAGACCCGACATCTCGGTGATGAAAGTCAGACACACAGC 60
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61 AGCTGGGTAGAGCTAGACCTGATAGATCTGAGCATGAGGAGGAGCTCCCTGGAGCT 120
61 AGCTGGGTAGAGCTAGACCTGATAGATCTGAGCATGAGGAGGAGCTCCCTGGAGCT 120
121 GCTCTGACCCGACGACATCTGCTCTGCTCCGCGCATGATACACGAGGTGCTGCTGCGCATC 180
121 GCTCTGACCCGACGACATCTGCTCTGCTCCGCGCATGATACACGAGGTGCTGCTGCGCATC 180
181 GAGGGGAGACCACTCTCCAGAGTATGCGCGCTCTCATATGAGGAGGAGCTCCCTGGAGCT 240
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601 CTTTGTGAGGAGACATCTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
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841 ATACATGCTTACTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
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901 AGTGGCTGAGTCCCTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
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961 AACAGATGCTGAGTCCCTCTGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
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1081 CCGAAGAGATGCGCAATTTTGAACCTCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
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RESULT 2
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LOCUS
DEFINITION
Homo sapiens gene for seven transmembrane helix receptor, complete cds, isolate:CBRC7TM_429.

AB065866
AB065866
AB065866.1 GI:21928996
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (isolate:CBRC7TM_429) DNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
REFERENCE

1 Suwa, M., Sato, T., Okouchi, I., Arita, M., Futami, K., Matsumoto, S.,
Tsutsumi, S., Aburatani, H., Asai, K. and Akiyama, Y.
Genome-wide discovery and analysis of human seven transmembrane
helix receptor genes
Unpublished
2 (bases 1 to 1441)

JOURNAL
TITLE
AUTHORS
REFERENCE
Suwa, M.
Direct Submission
Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research
Center (CBRC), National Institute of Advanced Industrial Science
and Technology (AIST); 2-41-6 Aomi Koto-Ku, Tokyo 135-0064, Japan
(E-mail:m-suwa@aist.go.jp, URL: <http://www.cbrc.jp/>,
Tel: 01-3-3599-8080, Fax: 01-3-3599-8081)

COMMENT
This sequence is a seven transmembrane helix receptor candidate
predicted from the whole human genome sequences using our automated
system that contains programs of gene
finding (Genedecoder), sequence search, motif-domain assignment and
transmembrane helix prediction.

And the sequence is submitted by the collaborative project between
[Computational Biology Research Center (CBRC), National Institute
of Advanced Industrial Science and Technology (AIST)] and [Genome
Science Division, Research Center for Advanced Science and
Technology (RCAST), University of Tokyo].

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Location/Qualifiers

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/evidence=not experimental
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BASE COUNT      299 a      405 c      377 g      360 t
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Query Match      99.4%; Score 1187.2; DB 9; Length 1441;
Best Local Similarity 99.6%; Pred. No. 1.2e-285;
Matches 1189; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCACAGCAACCCACACACAGAGACCCGATCCTGGTGATGAGTCAGACACRAGC 60
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DB 108 AGCTGGTGAAGTCTTAACGCTCAAGATAAGACATCTGTCATTTGGAGACTCCCTGGCT 167
QY 121 GCTCTGACCCGACACGCTGCTGCTCCCGCCATGTACAAAGGGTGTGCTGCCGATC 180
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QY 181 GAGGGGAGACACATCTCCAGAGTATCCGCGCTGCTCAATTGGGCTTTGGTGGG 240
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QY 421 GTGGGGCTTTCAGCTGGGCAATGAGGGCGGAGACATCGTGTCTTACGCTGTG 480
DB 468 GTGGGGCTTTCAGCTGGGCAATGAGGGCGGAGACATCGTGTCTTACGCTGTG 527
QY 481 GCTCGGACAGATATTTCAAGTGTGTCACCCCAACAGCGGTGAACCTATCTCAC 540
DB 528 GCTCGGACAGATATTTCAAGTGTGTCACCCCAACAGCGGTGAACCTATCTCAC 587
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QY 661 ATGAGTGGCCATGAGTGGACAGACATCATGTCCAGTGGAGTCTTTATGCCCCCTC 720
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QY 721 GGCATCATCTTATTTGCTCTTCAAGATTTGTTGAGGCTTGAAGCGAGGAGAGCTG 780
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QY 1141 TTCAAAGCAGTCTGATGGCAATGGATCCCAATTTGTTGATGGCAGCTGA 1194
DB 1188 TTCAAAGCAGTCTGATGGCAATGGATCCCAATTTGTTGATGGCAGCTGA 1241

RESULT 3
AX277635 1730 bp DNA linear PAT 01-NOV-2001
LOCUS AX277635
DEFINITION Sequence 1 from Patent WO0177320.
ACCESSION AX277635
VERSION AX277635.1 GI:16604811
KEYWORDS
SOURCE
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Xiao,Y.
Regulation of human hm74-like g protein coupled receptor
TITLE Patent: WO 0177320-A 1 18-0CN-2001;
JOURNAL Bayer Aktiengesellschaft (DE)
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Location/Qualifiers
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BASE COUNT 361 a 494 c 444 g 431 t
ORIGIN
Query Match 99.4%; Score 1187.2; DB 6; Length 1730;
Best Local Similarity 99.6%; Pred. No. 1.2e-285;
Matches 1189; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GCACAGCAACCCACACACAGAGACCCGATCCTGGTGATGAGTCAGACACRAGC 60
DB 311 GCAGCATCAACCCACACACAGAGACCCGATCCTGGTGATGAGTCAGACACRAGC 370
QY 61 AGCTGGTGAAGTCTTAACGCTCAAGATAAGACATCTGTCATTTGGAGACTCCCTGGCT 120
DB 371 AGCTGGTGAAGTCTTAACGCTCAAGATAAGACATCTGTCATTTGGAGACTCCCTGGCT 430
QY 121 GCTCTGACCCGACACGCTGCTGCTCCCGCCATGTACAAAGGGTGTGCTGCCGATC 180
DB 431 GCTCTGACCCGACACGCTGCTGCTCCCGCCATGTACAAAGGGTGTGCTGCCGATC 490
QY 181 GAGGGGAGACACATCTCCAGAGTATCCGCGCTGCTCAATTGGGCTTTGGTGGG 240
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QY 301 AGCAGCTTTACCTTTTCAATTTGACCGTGGTGAATTCCTCTTATGATCTGCTGCT 360
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RESULT 4
LOCUS AX299707 2331 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 3 from Patent WO0173029.
ACCESSION AX299707
VERSION AX299707.1 GI:17129251
KEYWORDS human.
SOURCE

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ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ye, J. C., Cravchik, A. C., di Francesco, V. C. and Beasley, E. M.
TITLE Isolated human g-protein coupled receptors, nucleic acid molecules
JOURNAL encoding human spcr proteins, and uses thereof
JOURNAL Patent: WO 0173029-A 3 04-0CT-2001,
PE Corporation (NY) (US)
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VERSION AF385432.1 GI:21205857
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2345)
AUTHORS Mao, M., Biery, M.C., Kobayashi, S.V., Schimmack, G.A., Ward, T.R.,
Scheller, J.M., Burchard, J., He, Y.D., Dai, H., Leonardson, A.,
Coffey, E., Stoughton, R. and Linsley, P.S.
T lymphocyte activation gene discovery using ink-jet microarrays
Unpublished
TITLE JOURNAL
REFERENCE 2 (bases 1 to 2345)
AUTHORS Mao, M., Biery, M.C., Kobayashi, S.V., Schimmack, G.A., Ward, T.R.,
Scheller, J.M., Burchard, J., He, Y.D., Dai, H., Leonardson, A.,
Coffey, E., Stoughton, R. and Linsley, P.S.
Direct Submission
TITLE JOURNAL
REFERENCE Submitted (25-MAY-2001) Research, Rosetta Pharmaceuticals, Inc., 12040
115th Ave NE, Kirkland, WA 98034, USA

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 REFERENCE 1 (bases 1 to 3612)
 AUTHORS Mao, M., Biery, M.C., Kobayashi, S.V., Schimmack, G.A., Ward, T.R.,
 Schelter, J.M., Burchard, J., He, Y.D., Dai, H., Leonardson, A.,
 Coffey, B., Stoughton, R. and Linsley, P.S.
 TITLE T lymphocyte activation gene discovery using ink-jet microarrays
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3612)
 AUTHORS Mao, M., Biery, M.C., Kobayashi, S.V., Schimmack, G.A., Ward, T.R.,
 Schelter, J.M., Burchard, J., He, Y.D., Dai, H., Leonardson, A.,
 Coffey, E., Stoughton, R. and Linsley, P.S.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAY-2001) Research, Rosetta Inpharmatics, Inc., 12040
 115th Ave NE, Kirkland, WA 98034, USA
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KEYWORDS SOURCE ORGANISM

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens

REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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 Sutton,A., Svatek,A., Taber,P., Tamezisa,A., Tamezisa,K., Tang,H.,
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 Usmani,K., Vaequez,L., Vera,V., Villalob,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G., and Gibbs,R.
 Direct Submission
 2 (bases 1 to 210805)
 Unpublished
 Direct Submission
 3 (bases 1 to 210805)
 Direct Submission
 Submitted (02-AUG-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Aug 1, 2002 this sequence version replaced gi:22024364.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Drafting Center Code: BCM
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: HAOK
 Center clone name: RP11-324E6
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Sequencing vector: M13;

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_drafi_data.html)
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 8 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

*	2240:	contig of 2240 bp in length
*	2241	2340: gap of unknown length
*	2341	5089: contig of 2749 bp in length
*	5090	5189: gap of unknown length
*	5190	13776: contig of 8587 bp in length
*	13777	13876: gap of unknown length
*	13877	37246: contig of 23370 bp in length
*	37247	37346: gap of unknown length
*	37347	58915: contig of 21569 bp in length
*	58916	59015: gap of unknown length
*	59016	78686: contig of 19671 bp in length
*	78687	78786: gap of unknown length
*	78787	141420: contig of 65634 bp in length
*	141421	141500: gap of unknown length
*	141521	210805: contig of 69285 bp in length

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FEATURES      Location/Qualifiers
source        1. .210805
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BASE COUNT	58093	47057	46299	58656	700
ORIGIN					

Query Match	99.4%	Score 1187.2;	DB 2;	Length 210805;
Best Local Similarity	99.6%;	Pred. No. 1.8e-25;		
Matches 1189;	Conservative	1;	Mismatches 4;	Indels 0;
				Gaps 0

Qy 1 GCACCGCAACCCACACACAGACCGGCATCTCGGTGATGAAGTCAGACACACG 60
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Qy 61 AGCTGGGTAGTGCCTAACGCTCAGATAGCATCTGTGCATTGTGGGGAATCCCTGGGCT 120
 Db 209107 AGCTGGGTAGTGCCTAACGCTCAGATAGCATCTGTGCATTGTGGGGAATCCCTGGGCT 209048

Qy 121 GCTTCACCCCGGACACTGCTGTCCCGCATGTACACGGGTCTGCTCCGCATC 180
 |||||
 Db 209047 GCTTCGACCCCGGACACTTGTCTCTGTCTCCCGCATGTACACGGGTCTGCTCCGCATC 208

27 181 GAGGGGGAACCAATCTCCAGGTGATGCCGCGCTGCATTTGGCCCTTTGTGCTGGGC 240
 Db 208987 GAGGGGGAACCAATCTCCAGGTGATGCCGCGCGCTGCATTTGGCCCTTTGTGCTGGGC 208928

241 GCACTAGGCATGGGGTCGCCCTGTGTGTTCTGCTTCCACATGAGACTGGAGCCC 300
 Db 208927 GCACTAGGCATGGGGTCGCCCTGTGTGTTCTGCTTCCACATGAGACTGGAGCCC 208868

501 AGCACTGTTACCTTTCAATTGGCGTGGCTGATTTCTCTATGATCTGCGTCCCT 360
Db 208867 AGCACTGTTACCTTTCAATTGGCGTGGCTGATTTCTCTATGATCTGCGTCCCT 208808

QY 361 TTTGGACAGACTATTACCTCAGACGTAGACACTGGGCTTTTGGGACATTCCCTGCCGA 420

QY 421 GTGGGGCTTTCACGTTGGCCATGAACAGGCGGGAGCATCGTGTCTTACCGTGTG 480
 Db 208747 GTGGGGCTTTCACGTTGGCCATGAACAGGCGGGAGCATCGTGTCTTACCGTGTG 208688

QY 481 GCTGCGGACAGTATTTCAAAGTGGTCCACCCACACACGCGTGAACTATCTCCACC 540
Db 208687 GCTGCGGACAGTATTTCAAAGTGGTCCACCCACACACGCGTGAACTATCTCCACC 2086288

QY 541 CCGGTGGCCGGCTGGATCGTCTGCACCTGTGGGCCCTGGTATCTCGGGAAcAGTGTAT 600
Db 208627 CCGGTGGCCGGCTGGATCGTCTGCACCTGTGGGCCCTGGTATCTCGGGAAcAGTGTAT 208568	

601	CTTTGCTGGAGAACCACTCTCTGCGTGCAGAGACGGCCGCTCTCTGGAGAGCTTCATC	660
208567	CTTTTGTCTGGAGAACCATCTCTGCGTGCAGAGACGGCCGCTCTCTGGAGAGCTTCATC	208508

Db 208507 ATGGAGTGGGCAATGGCTGGGCATGATCATATGTTCCAGCTGGAGTCTTTATGCCCCC 208448

Db 208447 GGATCATCTATTCTCTCTCAAGATTGTTGGAGCCGAGGCGAGGCACAGCTG 208388

Db 208387 GCCAGACAGGCTCGATGAAGAGCGACCCGGTTCATCATGGTGTGGCAATTGTTC 208328

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Db 208267 AGGCGCTGGATCCTCTGTCCATGGGGCCCTGCACATATACCCTTCAGCTTCACCTACATG 208208

Db 208207 AACAGCATGCTGATCCCCGTGTATTTATTTTCAAGCCCTCCTTCCCAATTCTAC 208148

Db 208147 AACAGCTCAAAATCTGCAGTCTGAACCAGCAGCCAGGACACTCAAAAACACAAGG 208088

Db 208087 CCGAAGAGATGCCAATTGCAACCTCGGTGCGAGAGTTCATCAGTGTGGCAATAGT 208028

Db 208027 TTCCAAAGCCAGTCTGATGGGCAATGGATCCCAATTGTGAGTGGCACATGA 207974

RESULTS 9	AX338374	1104 bp	DNA	linear	PAT 09-JAN-2002
LOCUS	AX338374				
DEFINITION	Sequence 4 from Patent WO0174904				

ACCESSION	AX338374
VERSION	AX338374.1
KEYWORDS	GI:18128871
SOURCE	human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1

AUTHORS	Majumder, K., Vernet, C.A., Casman, S.J., Wolenc, A.R., Spaderna, S.K., Padigar, M., Mishu, V.S., Tchernev, V.T., Spytek, K.A., Li, L., Baumgartner, J.C. and Gausev, V.
TITLE	Novel proteins and nucleic acids encoding same
JOURNAL	Patent: WO 0174904-A 4, 11-OCT-2001;
	Curegen Corporation (US)

FEATURES

source

Location/Qualifiers
1. .1104
/organism-"Homo sapiens"

BASE COUNT	216 a	318 c	295 g	275 t
ORIGIN				

Query Match	91.6%;	Score 1093.6;	DB 6;	Length 1104;
Best Local Similarity	99.6%;	Pred. No. 2.7e-262;		
Matches 1096;	Conservative	0;	Mismatches 4;	Indels 0;
			Gaps	0;

OY	95	GTGCAATTGGAGGAACTCCCTGGAGCTGCTTGACACCCGGACAACCTGCTGTGCCGCGCA	154
Db	1	GTGCAATTGGAGAACTCCCTGGAGCTGCTTGACACCCGGACAACCTGCTGTGCCGCGCA	60
OY	155	TGTAACAACGGGTCGTGCTGCGGATCGAGGGGAGACCACTCTCCAGGATGATGCCGCGC	214
Db	61	TGTAACAACGGGTCGTGCTGCGGATCGAGGGGAGACCACTCTCCAGGATGATGCCGCGC	120
OY	215	TGCTCATTTGGGCTTTTGTGCTGCGGAGCACTTAGGCAATGGGGTCGCCCTGTGAGTTTCT	274
Db	121	TGCTCATTTGGGCTTTTGTGCTGCGGAGCACTTAGCAATAGGGTCGCCCTGTGAGTTTCT	180
OY	275	GCTTCCACATGAAGACCTGGAAAGCCAGCACTGTTTACCTTTTCAATTTTGGCCGTGCTG	334
Db	181	GCTTCCACATGAAGACCTGGAAAGCCAGCACTGTTTACCTTTTCAATTTTGGCCGTGCTG	240
OY	335	ATTTCCTCTTATGATGTCGCTGCTTTTTCGACAGACTATTAACCTCAGACSTAGAACT	394
Db	241	ATTTCCTCTTATGATGTCGCTGCTTTTTCGACAGACTATTAACCTCAGACSTAGAACT	300
OY	395	GGGCGTTTTGGGGAATTTCCCGCCGAGATGGAGGCTTTCAAGTTGGCATAAGAACAGGCGC	454
Db	301	GGGCGTTTTGGGGAATTTCCCGCCGAGATGGAGGCTTTCAAGTTGGGCAATGAACAGGCGC	360
OY	455	GGAGCATGTTGCTTACGGTGTGGCTGCGGACAGTAATTTCAAAAGTGTCCACCCC	514
Db	361	GGAGCATGTTGCTTACGGTGTGGCTGCGGACAGTAATTTCAAAAGTGTCCACCCC	420
OY	515	ACCAAGCGGTGAACATACTTCCACCCGGGTGGCGGCTGGCATTCGTGTCAACCCGTGAG	574
Db	421	ACCAAGCGGTGAACATACTTCCACCCGGGTGGCGGCTGGCATTCGTGTCAACCCGTGAG	480
OY	575	CCCTGTGATCCTGGGAAACAGTGTATCTTTTGTGTGAGAAACATCTCTCGTCAAGAGA	634
Db	481	CCCTGTGATCCTGGGAAACAGTGTATCTTTTGTGTGAGAAACATCTCTCGTCAAGAGA	540
OY	635	CGGCGTCTCCTGTGAGAGCTTCACTAATGAGTGGCCAAATGGCTGGCAACGACATCATGT	694
Db	541	CGGCGTCTCCTGTGAGAGCTTCACTAATGAGTGGCCAAATGGCTGGCAATGACATCATGT	600
OY	695	TTCACCTGAGGTTCTTATATGCCCTGGGAAATCATTTATTTTCTCTCAAGATTGTTT	754
Db	601	TTCACCTGAGGTTCTTATATGCCCTGGGAAATCATTTATTTTCTCTCAAGATTGTTT	660
OY	755	GGAGCCTGAGGCGGAGGAGCAGCTGGCCAGACAGGCTCGAGTGAAGAAAGGCGACCCGT	814
Db	661	GGAGCCTGAGGCGGAGGAGCAGCTGGCCAGACAGGCTCGAGTGAAGAAAGGCGACCCGT	720
OY	815	TCAATCATGTGTGGCAATTGTGTTCACTCAATGCTACCTGCCCCAGCGTGTCTGCTAAGC	874
Db	721	TCAATCATGTGTGGCAATTGTGTTCACTCAATGCTACCTGCCCCAGCGTGTCTGCTAAGC	780
OY	875	TCTATTTTCCCTGGAAGGATGGCCCTCGAGTGGCTGCGATCCCTCTGTGTCANATGGAGCCGTG	934
Db	781	TCTATTTTCCCTGGAAGGATGGCCCTCGAGTGGCTGCGATCCCTCTGTGTCANATGGAGCCGTG	840
OY	935	ACATAACCTCAGCTTCACTCAATGAACAGACATGCTGATCCCTGTGTGTATTTATTTT	994
Db	841	ACATAACCTCAGCTTCACTCAATGAACAGACATGCTGATCCCTGTGTGTATTTATTTT	900
OY	995	CAAGCCCTCTTTCCCAATTTTACAAACAGCTCAAAATCTGCACTTGAATCCCAAC	1054

Accession	Sequence	Length
Dh 901	CAGAGCCCTCTTCCCAATTTCTACAAGAGTCGAAATCTGCAGTCTGAAACCGCAAGC	960
Qy 1055	AGCCAGAGCACTCAAAAACAAAGGCGGAGAGATGCGCAATTTTGAACCTCGGTGGCA	1114
Dh 961	AGCCAGAGCACTCAAAAACAAAGGCGGAGAGATGCGCAATTTTGAACCTCGGTGGCA	1020
Qy 1115	GGAGTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCG	1174
Dh 1021	GGAGTTGCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCG	1080
Qy 1175	ACATTGTTGAGTGGCACTGA	1194
Dh 1081	ACATTGTTGAGTGGCACTGA	1100

RESULT 10					
AX305131	AX305131	1083 bp	DNA	linear	PAT 11-DEC-2001
LOCUS					
DEFINITION	Sequence 11 from Patent WO0187937.				
ACCESSION	AX305131				
VERSION	AX305131.1	GI:17644766			

REFERENCE

¹ Patterson, C., Lu, D.A., Thornton, M., Lu, Y., Tribouley, C.M.,

TITLE G-protein coupled receptors
JOURNAL Patent: WO 0187937-A 11 22-NOV-2001;

FEATURES

Location/Qualifiers

BASE COUNT	211 a	314 c	288 g	270 c
ORIGIN				

Query Match	90.4%;	Score 1079.8;	DB 6;	Length 1083;
Best Local Similarity	99.8%;	Pred. No. 7.5e-259;		
Matches 1081; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

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Qy	172	TGCCGCATCGAGGGGGACACCATCTCCAGGTGATGCCGCGCTGTCATTTGAGCCTTT	231
Db	61	TGCCGCATCGAGGGGGACACCATCTCCAGGTGATGCCGCGCTGTCATTTGAGCCTTT	120
Qy	232	GTGCTGGGCGCATCTGAGCAATGGGGGTGGCCCTGTGTGGTTTCGTCTCCACATGAAACCC	291
Db	121	GTGCTGGGCGCATGAGCAATGGGGGTGGCCCTGTGTGGTTTCGTCTCCACATGAAACCC	180
Qy	292	TGGAAGCCGACAGCTGTTACCTTTTCAATTTGGCCGTGGCTGATTTTCCTCTTATATC	351
Db	181	TGGAAGCCGACAGCTGTTACCTTTTCAATTTGGCCGTGGCTGATTTTCCTCTTATATC	240
Qy	352	TGCCTGCTTTTCGACAGACTATTACTCAGACGTAGACACTGGGCTTTTGGGGACATT	411
Db	241	TGCCTGCTTTTCGACAGACTATTACTCAGACGTAGACACTGGGCTTTTGGGGACATT	300
Qy	412	CCCTCCGACATGGGGGCTTTCACGTTGGCCATGAAACGGGCGGGAGCATGTTTCCTT	471
Db	301	CCCTCCGACATGGGGGCTTTCACGTTGGCCATGAAACGGGCGGGAGCATGTTTCCTT	360
Qy	472	ACGGTGTGTGCTGCGGACAGGATTTCAAAATGTGTCCACCCCAACAAGCGGTGAACACT	531
Db	361	ACGGTGTGTGCTGCGGACAGGATTTCAAAATGTGTCCACCCCAACAAGCGGTGAACACT	420

QY 532 ATCTCAGCCCGGCTGGCGGCTGGCATTCGTCTGACACCTGTGGGCCCTGTGATCCTGGGA 591
Db 421 ATCTCAGCCCGGCTGGCGGCTGGCATTCGTCTGACACCTGTGGGCCCTGTGATCCTGGGA 480
QY 592 ACAGGTATCTTTTCTGTGGAGAACATCTCTGCGGCGAGAGACCGCCGCTCTCTGTAG 651
Db 481 ACAGGTATCTTTTCTGTGGAGAACATCTCTGCGGCGAGAGACCGCCGCTCTCTGTAG 540
QY 652 AGCTTCATCATGAGTGGCCCAATGAGCTGGAGACGACATCATGTTCCAGCTGAGTCTTT 711
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QY 772 CAGCAGCTGGCCAGACAGGCTCGGATGGAAGAGGAGCCCGTTTCATCATGAGTGGGA 831
Db 661 CAGCAGCTGGCCAGACAGGCTCGGATGGAAGAGGAGCCCGTTTCATCATGAGTGGGA 720
QY 832 ATGTGTTCATCATACATGCTACCTGCGCAGCGTGTCTGTAAGTCTTATTTCTCTGAG 891
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QY 1012 AAATTTCTACAAAGCTCAAAATCTGAGTGAAGCCCAAGCAGCAGCACTCAAAA 1071
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Db 1081 TGA 1083

RESULT 11
AX38371 1050 bp DNA linear PAT 09-JAN-2002
LOCUS AX38371
DEFINITION Sequence 1 from Patent WO0174904.
ACCESSION AX38371
VERSION AX38371.1 GI:18128869
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Majumder, K., Verne, C.A., Casman, S.J., Wolenc, A.R., Spaderna, S.K.,
Baumgartner, J.C., and Gusev, V.Y.,
Novel proteins and nucleic acids encoding same
Patent: WO 0174904-A 1 11-OCT-2001;
Curagen Corporation (US)
FEATURES
source 1.1050
Location/Qualifiers
1.1050
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 211 a 299 c 279 g 261 t

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Query Match 87.5%; Score 1044.4; DB 6; Length 1050;
Best Local Similarity 99.9%; Pred. No. 5.2e-250;
Matches 1045; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 209 CGCCGCTGCTCATTTGTGCTTTGTGCTGGCGCATAGGAGATGGAGTGGCTGTGTG 268
Db 61 CGCCGCTGCTCATTTGTGCTTTGTGCTGGCGCATAGGAGATGGAGTGGCTGTGTG 120
QY 269 GTTTCGCTTCCACATGAGACCTGGAACCCAGACATGTTTAACTTTCAATTTGGCCG 328
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QY 329 TGGCTGATTTCTCTTATGATCTGCTGCTTTTCGACAGACTATTACCTGACAGTA 388
Db 181 TGGCTGATTTCTCTTATGATCTGCTGCTTTTCGACAGACTATTACCTGACAGTA 240
QY 389 GACACTGGGCTTTTGGGACATTCCTGCGAGTGGGCTCTTCACTTTGGCCATGAA 448
Db 241 GACACTGGGCTTTTGGGACATTCCTGCGAGTGGGCTCTTCACTTTGGCCATGAA 300
QY 449 GGGCGGAGACATCGTGTCTTACGATGTGGCTGGGACAGATTTTCAAGTGTTC 508
Db 301 GGGCGGAGACATCGTGTCTTACGATGTGGCTGGGACAGATTTTCAAGTGTTC 360
QY 509 ACCCCACACACGCGGTGAACATCTATCTCCACCCGGGTGGGCTTGGCATCTGACACC 568
Db 361 ACCCCACACACGCGGTGAACATCTATCTCCACCCGGGTGGGCTTGGCATCTGACACC 420
QY 569 TGTGGGCTCTGCTCATCTCTGGGACAGTGTATCTTTTGTGAGAACATCTCTGCTGC 628
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QY 629 AAGAGCGGCGCTCTCTGTGAGACCTCATCATGAGTGGGCAATGGCTGGACGCA 688
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QY 869 CTAGACTTATTTCTCTGAGCGGTGCTGAGTGGCTGGCATCTCTGTCTCATGAGG 928
Db 721 CTAGACTTATTTCTCTGAGCGGTGCTGAGTGGCTGGCATCTCTGTCTCATGAGG 780
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QY 989 ATTTTTCAGCCCTCTCTTCCAAATTTTCAACAAGCTCAAAATCTGAGTGTGAAC 1048
Db 841 ATTTTTCAGCCCTCTCTTCCAAATTTTCAACAAGCTCAAAATCTGAGTGTGAAC 900
QY 1049 CCAAGCAGCAGGACATCTCAAAAACAAAGAGCGGAGAGAGATCCAAATTTGAACTCG 1108
Db 901 CCAAGCAGCAGGACATCTCAAAAACAAAGAGCGGAGAGAGATCCAAATTTGAACTCG 960
QY 1109 GTGCGAGAGTGTGATGAGTGGCAATGTTTCCAAAGCAGTCTGATGGGCAATGGG 1168
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QY 1169 ATCCCAAGTTGTTGAGTGCGACTGA 1194
DB 1021 ATCCCAAGTTGTTGAGTGCGACTGA 1046

RESULT 12
AX38373 1050 bp DNA linear PAT 09-JAN-2002
LOCUS Sequence 3 from Patent WO0174904.
DEFINITION AX38373
ACCESSION AX38373
VERSION AX38373.1 GI:18128870
KEYWORDS
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 Majumder, K., Vernet, C.A., Casman, S.J., Wolenc, A.R., Spaderna, S.K.,
Padigaru, M., Mishra, V.S., Tchernev, V.I., Spytek, K.A., Li, L.,
Baumgartner, J.C. and Gusev, V.Y.
Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0174904-A 3 11-OCT-2001;
Curagen Corporation (US)
FEATURES
Source 1..1050
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 211 a 298 c 279 g 262 t
ORIGIN

Query Match 87.4%; Score 1043.4; DB 6; Length 1050;
Best Local Similarity 99.9%; Pred. No. 9.3e-250;
Matches 1044; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 150 CGCAGTGTACACAGGGTCTGCTGCGCATTCGAGGGGAGACACATCTCCAGGTGATGCC 209
DB 2 CGCAGTGTACACAGGGTCTGCTGCGCATTCGAGGGGAGACACATCTCCAGGTGATGCC 61

QY 210 GCGGCTGCTCATTTGAGCCCTTTTGTGCTGGGCGCATAGGCAATGGGGTGGCTGTGTGG 269
DB 62 GCGGCTGCTCATTTGAGCCCTTTTGTGCTGGGCGCATAGGCAATGGGGTGGCTGTGTGG 121

QY 270 TTTCTGTTCCACATGAGAGCCTGGAAGCCAGACAGTCTTCAATTTGGACCT 329
DB 122 TTTCTGTTCCACATGAGAGCCTGGAAGCCAGACAGTCTTCAATTTGGACCT 181

QY 330 GGGTGAATTTCTCTTATGATCTGCTGCTTTTGGACAGATTAATCTGACAGTAG 389
DB 182 GGGTGAATTTCTCTTATGATCTGCTGCTTTTGGACAGATTAATCTGACAGTAG 241

QY 390 ACACTGGGCTTTTGGGAGACATTCCTGCGAGAGGGGCTTTCAAGTGGCCATGAAAG 449
DB 242 ACACTGGGCTTTTGGGAGACATTCCTGCGAGAGGGGCTTTCAAGTGGCCATGAAAG 301

QY 450 GGGCGGAGAGATGCTGTTCTCTTACGGTGGTGGGCGGAGACAGTATTTCAAGTGGTCA 509
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QY 510 CCCCACACAGCGGTGAACATATCTTCACCCGGGTGGCGGTGGCATGCTTGCACCTT 569
DB 362 CCCCACACAGCGGTGAACATATCTTCACCCGGGTGGCGGTGGCATGCTTGCACCTT 421

QY 570 GTGGGCTCTGTATCTCTGGGAGAGATATCTTTTGTGGAAGAACATCTCTGGGTGA 629
DB 422 GTGGGCTCTGTATCTCTGGGAGAGATATCTTTTGTGGAAGAACATCTCTGGGTGA 481

QY 630 AGAGACGCGCTCTCTGTGAGAGCTTCATCATGAGATCGGCAATGGCTGGACAGAT 689
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DB 902 CAGCAGCCAGAGACTCAAAAACAAAGGCGGAGAGATGCAATTTGCAACCTGG 961
QY 1110 TCGCAGAGTTGATCATGATGAGTGGCAATGTTTCCAAAGCAGTGTGATGGCAATGGGA 1169
DB 962 TCGCAGAGTTGATCATGATGAGTGGCAATGTTTCCAAAGCAGTGTGATGGCAATGGGA 1021
QY 1170 TCCCAATTTGATGAGTGGCACTGA 1194
DB 1022 TCCCAATTTGATGAGTGGCACTGA 1046

RESULT 13
AX395171 1041 bp DNA linear PAT 18-MAY-2002
LOCUS Sequence 3 from Patent WO0218579.
DEFINITION AX395171
ACCESSION AX395171
VERSION AX395171.1 GI:21066221
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 Glucksmann, M.A.
57242, a novel human g protein-coupled receptor family member and
uses thereof
JOURNAL Patent: WO 0218579-A 3 07-MAR-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Source 1..1041
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 208 a 295 c 278 g 260 t
ORIGIN

Query Match 87.2%; Score 1041; DB 6; Length 1041;
Best Local Similarity 100.0%; Pred. No. 3.7e-249;
Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 ATGTACAAGGGTGTGCTGCGCATGAGGGGAGACATCTTCCAGGTGATGCGCG 213
DB 1 ATGTACAAGGGTGTGCTGCGCATGAGGGGAGACATCTTCCAGGTGATGCGCG 60
QY 214 CTGCTCATTTGGGCTTTTGTGCTGGGCGCACTAGGCAATGGGGTGGCTGTGTTTC 273
DB 61 CTGCTCATTTGGGCTTTTGTGCTGGGCGCACTAGGCAATGGGGTGGCTGTGTTTC 120
QY 274 TGTCTTCCATGAGAGCTGGAAGCCAGACTTATACCTTTTCAATTTGGCGTGGCT 333

```

Db 121 TGCTTCACATGACAGACCTGGAGAGCCGACGACTGTTTACCTTTTCAATTTGGCCGTGGCT 180
 QY 334 GATTTCCTCTTATGATCTGCTGCTTTTGGAGACAGACTATTAACCTCAGACGTAGACAC 393
 Db 181 GATTTCCTCTTATGATCTGCTGCTTTTGGAGACAGACTATTAACCTCAGACGTAGACAC 240
 QY 334 TGGGCTTTTGGGAGACATTCCTGCGAGTGGGGCTTTTCACTTTGGCCATGAGAGGCC 453
 Db 241 TGGGCTTTTGGGAGACATTCCTGCGAGTGGGGCTTTTCACTTTGGCCATGAGAGGCC 300
 QY 454 GGGAGCATGCTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 513
 Db 301 GGGAGCATGCTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 514 CACCAAGCGGTGAACATCTATCCACCCGGGTGGGGGTGGAGTGGAGTGGAGTGGAGTGGAG 573
 Db 361 CACCAAGCGGTGAACATCTATCTCACCCGGGTGGGGGTGGAGTGGAGTGGAGTGGAGTGGAG 420
 QY 574 GCGCTGCTATCTGGGAGACAGTGTATTTTGGTGGAGAACATCTCTGCTGCTGCTGCTGCTGCT 633
 Db 421 GCGCTGCTATCTGGGAGACAGTGTATTTTGGTGGAGAACATCTCTGCTGCTGCTGCTGCTGCT 480
 QY 634 AGCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 693
 Db 481 AGCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 694 TTCCAGCTGAGATTCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
 Db 541 TTCCAGCTGAGATTCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 754 TGGAGCTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 813
 Db 601 TGGAGCTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
 QY 814 TTCAATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 873
 Db 661 TTCAATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 QY 874 CTCTATTTCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 933
 Db 721 CTCTATTTCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 QY 934 CACATAACCTCAGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 993
 Db 781 CACATAACCTCAGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 840
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 QY 1054 CACCAAGGAGCACTCAAAAACAAAGGCGGAGAGAGAGTGGCAATTTTCAAACTCGGTGGC 1113
 Db 901 CACCAAGGAGCACTCAAAAACAAAGGCGGAGAGAGTGGCAATTTTCAAACTCGGTGGC 960
 QY 1114 AGGAGTTGATCAGTGTGGCAATAGTTTCAAAAGCAGTGTGAGGCAATGGAGTGGC 1173
 Db 961 AGGAGTTGATCAGTGTGGCAATAGTTTCAAAAGCAGTGTGAGGCAATGGAGTGGC 1020
 QY 1174 CACATTTGATGAGGCACTGA 1194
 Db 1021 CACATTTGATGAGGCACTGA 1041

RESULT 14
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 LOCUS AX147834 1041 bp DNA linear PAT 08-JUN-2001
 DEFINITION Sequence 79 from Patent WO0136473.
 ACCESSION AX147834
 VERSION AX147834.1 GI:14346838
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 1 (bases 1 to 1041)
 AUTHORS
 Vogeli, G., Wood, U.S., Parodi, L.A., Hiebsch, R.R., Lind, P.,
 Slightom, J., Schellin, K.A., Kayes, P.S., Bannigan, C.M., Ruff, V.,
 Seifritz, T., and Huff, R.M.
 TITLE
 Novel 9 protein-coupled receptors
 JOURNAL
 Parent: WO 0136473-A 79 25-MAY-2001;
 PHARMACIA & UPJOHN COMPANY (US)
 FEATURES
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 1. 1041
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 208 a 294 c 278 g 261 t
 ORIGIN
 Query Match 87.1%; Score 1039.4; DB 6; Length 1041;
 Best Local Similarity 99.9%; Pred. No. 9.3e-249;
 Matches 1040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 154 ATGTACAAAGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 213
 Db 1 ATGTACAAAGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 QY 214 CTGCTCATTTGAGGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 273
 Db 61 CTGCTCATTTGAGGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 QY 274 TGCTTCAATGAGAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 333
 Db 121 TGCTTCAATGAGAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 QY 334 GATTTCCTCTTATGATCTGCTGCTTTTGGAGACAGACTATTAACCTCAGACGTAGACAC 393
 Db 181 GATTTCCTCTTATGATCTGCTGCTTTTGGAGACAGACTATTAACCTCAGACGTAGACAC 240
 QY 394 TGGGCTTTTGGGAGACATTCCTGCGAGTGGGGCTTTTCACTTTGGCCATGAGAGGCC 453
 Db 241 TGGGCTTTTGGGAGACATTCCTGCGAGTGGGGCTTTTCACTTTGGCCATGAGAGGCC 300
 QY 454 GGGAGCATGCTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 513
 Db 301 GGGAGCATGCTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 514 CACCAAGCGGTGAACATCTATCCACCCGGGTGGGGGTGGAGTGGAGTGGAGTGGAGTGGAG 573
 Db 361 CACCAAGCGGTGAACATCTATCCACCCGGGTGGGGGTGGAGTGGAGTGGAGTGGAGTGGAG 420
 QY 574 GCGCTGCTATCTGGGAGACAGTGTATTTTGGTGGAGAACATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 633
 Db 421 GCGCTGCTATCTGGGAGACAGTGTATTTTGGTGGAGAACATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 634 AGCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 693
 Db 481 AGCGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 694 TTCCAGCTGAGATTCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
 Db 541 TTCCAGCTGAGATTCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 754 TGGAGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 813
 Db 601 TGGAGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
 QY 814 TTCAATCAGTGTGGCAATAGTTTCAAAAGCAGTGTGAGGCAATGGAGTGGC 873
 Db 661 TTCAATCAGTGTGGCAATAGTTTCAAAAGCAGTGTGAGGCAATGGAGTGGC 720
 QY 874 CTCTATTTCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 933
 Db 721 CTCTATTTCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 QY 934 CACATAACCTCAGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 993

Db 781 CACATTAACCTCAGCTTACCTACCTAGCAAGCATGCTGATCCCTGCTGATTTATTTT 840
 QY 994 TCAGCCCCCTCTTCTCCCAATTTCTACAAACAAGCTCAAAATCTGAGTCTGAAACCCAG 1053
 Db 841 TCAGCCCCCTCTTCTCCCAATTTCTACAAACAAGCTCAAAATCTGAGTCTGAAACCCAG 900
 QY 1054 CAGCCAGACATCTCAAAAACAAAGGCCGAGAGATGCCAATTTGCAACTGCGTGC 1113
 Db 901 CAGCCAGACATCTCAAAAACAAAGGCCGAGAGATGCCAATTTGCAACTGCGTGC 960
 QY 1114 AGAGTTCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGCAATGGGATCCC 1173
 Db 961 AGAGTTCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGCAATGGGATCCC 1020
 QY 1174 CACATTTGAGTGGCACTGA 1194
 Db 1021 CACATTTGAGTGGCACTGA 1041

RESULT 15
 AX148182 1041 bp DNA linear PAT 08-JUN-2001
 LOCUS AX148182 Sequence 23 from Patent WO0136471.
 DEFINITION AX148182
 ACCESSION AX148182
 VERSION AX148182.1 GI:14347084
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Chien, R., Dang, H.T. and Lowitz, K.P.
 Endogenous and non-endogenous versions of human g protein-coupled
 receptors
 Patent: WO 0136471-A 23 25-MAY-2001;
 Arena Pharmaceuticals, Inc. (US)
 Location/Qualifiers
 source 1..1041
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 208 a 294 c 278 g 261 t
 ORIGIN

Query Match 87.1%; Score 1039.4; DB 6; Length 1041;
 Best Local Similarity 99.9%; Pred. No. 9.3e-249;
 Matches 1040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 154 ATGTACAACGGGTGCTGCTGCTCCGATCGAGGGGAGACACCATCTCCAGGTGATGCCGCG 213
 Db 1 ATGTACAACGGGTGCTGCTGCTCCGATCGAGGGGAGACACCATCTCCAGGTGATGCCGCG 60
 QY 214 CTGCTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 273
 Db 61 CTGCTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
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 Db 121 TGCTTCACATGAAGACCTGGAAGCCAGACATGTTTACCTTTCAATTTGGCGTGCCT 180
 QY 334 GATTTCCTCTTATGATCTGCTGCTGCTTTCGACAGACTATTACTCAGACGTAGACAC 393
 Db 181 GATTTCCTCTTATGATCTGCTGCTGCTTTCGACAGACTATTACTCAGACGTAGACAC 240
 QY 394 TGGGCTTTGGGAGCATTTCCCTGCGAGTGGGGCTTTTCACTGTTGGCCATGAACAGGGCC 453
 Db 241 TGGGCTTTGGGAGCATTTCCCTGCGAGTGGGGCTTTTCACTGTTGGCCATGAACAGGGCC 300
 QY 454 GGGAGCATCGGTCTCTTACGAGTGTGGCTGCGGACAGATATTCAAAGTGTCAACCCC 513
 Db 301 GGGAGCATCGGTCTCTTACGAGTGTGGCTGCGGACAGATATTCAAAGTGTCAACCCC 360
 QY 514 CACCAACGGGTGAACACTATCTCCACCCGGGTGGCGGCTGCACTGCTGCACTGCTG 573

Db 361 CACACAGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGCACTGCTGCACTGCTG 420
 QY 574 GCGCTGTGATCTCTGGGAACAGTATCTTTTGTCTGGAAGAACATCTCTGCGTGAAGAG 633
 Db 421 GCGCTGTGATCTCTGGGAACAGTATCTTTTGTCTGGAAGAACATCTCTGCGTGAAGAG 480
 QY 634 ACAGCGGTCTCTGAGAGCTTTCATGAGAGTGGCCAAATGGCTGCAACATCATG 693
 Db 481 ACAGCGGTCTCTGAGAGCTTTCATGAGAGTGGCCAAATGGCTGCAACATCATG 540
 QY 694 TTCAGCTGAGTCTTTTATGCCCCCTGCGCATCATCTTATTTTGTCTCTTCAAGATGTT 753
 Db 541 TTCAGCTGAGTCTTTTATGCCCCCTGCGCATCATCTTATTTTGTCTCTTCAAGATGTT 600
 QY 754 TGGAGCTGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 813
 Db 601 TGGAGCTGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
 QY 814 TTCATCATGAGTGTGGCAATGTTGTTTATCATCATGCTACCTGCCAGCGTGTCTGTA 873
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 QY 874 CTCTATTTCTCTGAGCGGTGCTGAGTGGCTGAGTGGCTGAGTGGCTGAGTGGCTGAG 933
 Db 721 CTCTATTTCTCTGAGCGGTGCTGAGTGGCTGAGTGGCTGAGTGGCTGAGTGGCTGAG 780
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 QY 994 TCAAGCCCCCTCTTCTCCCAATTTCTACAAACAAGCTCAAAATCTGCACTGTAAGCCCAAG 1053
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 Db 901 CAGCCAGACATCTCAAAAACAAAGGCCGAGAGATGCCAATTTGCAACTGCGTGC 960
 QY 1114 AGAGTTCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGCAATGGGATCCC 1173
 Db 961 AGAGTTCATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGCAATGGGATCCC 1020
 QY 1174 CACATTTGAGTGGCACTGA 1194
 Db 1021 CACATTTGAGTGGCACTGA 1041

Search completed: April 3, 2003, 22:11:51
 Job time : 3810 secs

XX XX
EN WO200218579-A2.
XX 07-MAR-2002.
XX 29-AUG-2001; 2001WO-US26882.
XX 29-AUG-2000; 2000US-228409P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Glucksmann MA;
XX WPI, 2002-479433/51.
XX P-FSDB; AAE24354.
XX
XX Human G protein coupled receptor nucleic acid and polypeptide
XX molecules, designated 57242, useful for diagnosing, preventing or
XX treating aberrant lipogenesis or aberrant lipolysis, obesity, diabetes
XX or bone disorders (e.g. osteoporosis) -
XX
XX Claim 1; Page 111-112; 114pp; English.
XX
XX The invention relates to G protein coupled receptor (GPCR) family
XX member, 57242 and its corresponding nucleic acid sequence. The 57242
XX nucleic acid and polypeptide are useful for diagnosing, preventing
XX or treating a subject having or at risk of developing a metabolic
XX disorder, particularly a disorder associated with aberrant lipogenesis
XX or aberrant lipolysis, obesity or diabetes. The 57242 DNA and protein
XX are also useful for treating a subject having bone disorder, where
XX the disorder is osteoporosis or a disorder associated with aberrant
XX osteogenesis or aberrant bone resorption. These diseases include
XX obesity, diabetes, hyperlipidaemia, overweight, anorexia or cachexia.
XX The 57242 DNA and protein are also useful for treating a subject
XX having haematopoietic disorders, autoimmune disorders e.g. psoriasis
XX and multiple sclerosis, brain disorders, degenerative diseases e.g.
XX Alzheimer's disease and pick disease and disorders involving heart.
XX The 57242 nucleic acid and polypeptide are also useful for modulating
XX adipocyte activity such as hyperplastic growth, hypertrophic growth
XX or lipogenesis. The 57242 DNA is used in gene therapy. The present
XX sequence is human 57242 cDNA.
XX
XX Sequence 1194 BP; 240 A; 349 C; 318 G; 286 T; 1 other;
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Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 GAGGGGAGACCAATCTCCAGTGAATGCCGCGCTGCTCAATTTGGCTTTGTGTGGGC 240
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DB 361 TTTCGACAGACTTATTAATCTGACAGTGAACAATGGGCTTTTGGGACATTTCTCTGCGCA 420
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DB 421 GTGGGCTCTTCAACGTTGGCCATGAACAGGGGCGGAGATGCTGTCCTTACGGTGGTG 480
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DB 541 CGGATGCGGCTGGCATGCTGTGACCTGTGGGCTGTGTATCTCTGGGAACATGTAT 600
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DB 601 CTTTTCGTGAGAACCATCTGCGGCAAGAGACGGGCGCTCCCTGATGAGACTTATC 660
QY 661 ATGAGTGGCCCAATGCTGGGACGACATCATGTTCCAGCTGAGATTCTTATGCCCCTC 720
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QY 721 GGCATCATCTTATTTTGTCTCTTCAAGATTGTTGAGGCTTGAAGCGGAGAGACGCTG 780
DB 721 GGCATCATCTTATTTTGTCTCTTCAAGATTGTTGAGGCTTGAAGCGGAGAGACGCTG 780
QY 781 GCCAGACAGGCTGGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 GCCAGACAGGCTGGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 ATCAATGATCTTACCTGCGCACAGCGTGTCTGTAAGCTTATTTCTCTGACCGTCCCTG 900
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DB 961 AACGAGTGGTGGATCCCTGCTGTATTTTCAAGCCCTCTTCCCAATTTCTAC 1020
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DB 1021 AACAGCTCAAAATCTGAGTGTGAACCCAGACAGCGACATCAAAACACAAAG 1080
QY 1081 CCGAAGAGATGCCAATTTTGAACCTGCGGAGAGGTTGATCATGTGGCAATTAAG 1140
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QY 1141 TTCCAAAGCCAGTGTGATGGCAATGGGATCCCAATTTGTGATGAGTGA 1194
DB 1141 TTCCAAAGCCAGTGTGATGGGCAATGGGATCCCAATTTGTGATGAGTGA 1194
RESULT 2
AAS18501
ID AAS18501 standard; cDNA; 1730 BP.
XX AAS18501;
XX 26-FEB-2002 (first entry)
XX
XX cDNA encoding HM74-like G-protein coupled receptor (GPCR).
XX
XX HM74-like GPCR; G-protein coupled receptor; antibacterial; fungicide;
XX protozoacide; analgesic; cyostatic; neuroleptic; mootropic;
XX anticonvulsant; tranquilizer; viral infection; pain; cancer; anorexia;
XX bulimia; asthma; central nervous system disease; CNS disease;
XX cardiovascular disease; hypertension; hyperextension; angina pectoris;
XX myocardial infarction; urinary retention; osteoporosis; ulcer; asthma;
XX inflammation; allergy; benign prostatic hypertrophy; multiple sclerosis;

ID AAS12582 standard; DNA; 2331 BP.
 XX
 XX AAS12582;
 AC
 DT 19-DEC-2001 (first entry)
 XX
 DE Gene encoding novel human G protein-coupled receptor (GPCR).
 XX
 KM Human; G-protein coupled receptor; GPCR; chemokine receptor; protease;
 KM hyperproliferative disorder; neurological disorder; psychiatric disease;
 KM inflammatory disorder; respiratory disorder; gene therapy; ds.
 XX
 OS Homo sapiens.
 XX
 PN MO200173029-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001MO-US09522.
 XX
 PR 27-MAR-2000; 2000US-192419P.
 PR 06-SEP-2000; 2000US-230459P.
 PR 20-SEP-2000; 2000US-0666535.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Ye J, Cravchik A, Di Francesco V, Beasley EM;
 XX
 DR WPI; 2001-616503/71.
 XX
 PT Novel human G-protein coupled receptor proteins and nucleic acid
 PT molecules encoding the protein for use in developing human therapeutics
 PT and diagnostic compositions and for identifying modulators of the
 PT protein -
 XX
 PS Claim 23; Fig 3; 66pp; English.
 XX
 CC The present invention relates to the isolation of a novel human G-protein
 CC coupled receptor (GPCR) which is related to the chemokine receptor
 CC subfamily. The CDNA and gene sequences encoding for GPCR are also
 CC given in the invention. The sequences of the invention are useful
 CC for diagnosing and treating diseases or conditions mediated by human
 CC proteases. Such diseases include hyperproliferative disorders
 CC (e.g. hyperplasia), neurological disorders (e.g. Parkinson's disease),
 CC psychiatric diseases (e.g. schizophrenia), inflammatory disorders
 CC (e.g. diabetes) and respiratory disorders (e.g. adult respiratory
 CC distress syndrome, ARDS). The GPCR protein is also useful for identifying
 CC a modulator of the expression of the protein. It also serves as a target
 CC for identifying agents for use in mammalian therapeutic applications,
 CC e.g. a human drug, particularly modulating a biological or pathological
 CC response in a cell or tissue that expresses the protein, in biological
 CC assays related to GPCRs that are related to members of the chemokine
 CC receptor subfamily, in drug screening assays and in competition binding
 CC assays. GPCR is also useful in diagnosing a disease or predisposition to
 CC a disease mediated by the peptide, in pharmacogenomic analysis. The
 CC polynucleotide sequences can also be used in gene therapy. The present
 CC sequence represents the human GPCR gene sequence of the invention.
 XX
 SQ Sequence 2331 BP; 497 A; 620 C; 592 G; 622 T; 0 other;
 Query Match 99.4%; Score 1187.2; DB 22; Length 2331;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1189; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 278 GCTGTGCAACCCGGACACTTGTCTGTCCCGCCAGTGAACAAGGATGCTGCGGCATC 337
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 QY 301 AGCACTGTTTACCTTTTCAATTTGGCGGTGATTTTCTCTTATGATCTGCTGCT 360
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 Db 878 GGCATCATCTTATTTTGTCTCTTCAAGATTTGTTGAGCGCTGAGCGGAGGACGACGCTG 937
 QY 781 GCCAGACAGGCTCGGATGAAGAAGAGGACCGGTTTCATCATGTGGTGGCAATTTGTTC 840
 Db 938 GCCAGACAGGCTCGGATGAAGAAGAGGACCGGTTTCATCATGTGGTGGCAATTTGTTC 997
 QY 841 ATCAATGCTTACCTGCCAGCGGTGTGCTTGAAGCTTATTTCTCTGACGCTGCCCTCG 900
 Db 998 ATCAATGCTTACCTGCCAGCGGTGTGCTTGAAGCTTATTTCTCTGACGCTGCCCTCG 1057
 QY 901 AGTGCCTGCGATCCCTCTGTCACAGGGGCGCTGACATAACCTCAGCTTACCTACATG 960
 Db 1058 AGTGCCTGCGATCCCTCTGTCACAGGGGCGCTGACATAACCTCAGCTTACCTACATG 1117
 QY 961 AACGACATGCTGAATCCCTGCTGTATTTATTTTCAAGCCCTCTTCCCAATTTCTAC 1020
 Db 1178 AACGACATGCTGAATCCCTGCTGTATTTATTTTCAAGCCCTCTTCCCAATTTCTAC 1237
 QY 1081 CCGGAAAGAGTCCCAATTTTGAACCTGTGTGCAAGAGTTGATCAATGTGGCAATTAAT 1140
 Db 1238 CCGGAAAGAGTCCCAATTTTGAACCTGTGTGCAAGAGTTGATCAATGTGGCAATTAAT 1297
 QY 1141 TTCCAAAGCCAGTCTGATGGGCAATGGGATCCCACTTGTGATGGGCACTGA 1194
 Db 1298 TTCCAAAGCCAGTCTGATGGGCAATGGGATCCCACTTGTGATGGGCACTGA 1351

RESULT 4

ABA81531
 ID ABA81531 standard; DNA; 1104 BP.
 AC ABA81531;
 DT 28-JAN-2002 (first entry)
 XX
 DE Human GPCRic polynucleotide SEQ ID NO 4.
 XX
 KW Human; GPCR; G-coupled protein-receptor; cardiant; antiarteriosclerotic;
 KW anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
 KW asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;
 KW infection; human immunodeficiency virus; HIV; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200174904-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10241.
 XX
 PR 31-MAR-2000; 2000US-193664P.
 PR 05-APR-2000; 2000US-194614P.
 PR 06-APR-2000; 2000US-195063P.
 PR 06-APR-2000; 2000US-195067P.
 PR 06-APR-2000; 2000US-195067P.
 PR 06-APR-2000; 2000US-195069P.
 PR 06-APR-2000; 2000US-195070P.
 PR 06-APR-2000; 2000US-195510P.
 PR 21-JUL-2000; 2000US-219855P.
 PR 27-JUL-2000; 2000US-221284P.
 PR 28-JUL-2000; 2000US-221325P.
 PR 11-AUG-2000; 2000US-224588P.
 PR 11-OCT-2000; 2000US-239613P.
 PR 18-JAN-2001; 2001US-262508P.
 PR 23-JAN-2001; 2001US-263433P.
 PR 23-JAN-2001; 2001US-263604P.
 PR 30-JAN-2001; 2001US-265161P.
 PR 29-MAR-2001; 2001US-0823172.
 XX
 (CURA-) CURAGEN CORP.
 PA
 PI Majumder K, Vernet CAM, Casman SJ, Wolenc AR, Spaderma SK,
 PI Padigaru M, Mishra VS, Tchernev VT, Spytek KA, Li L;
 PI Baumgartner JC, Gusev VY;
 DR MPI; 2001-639351/73.
 DR P-PSDB; ABA81531.
 XX
 PT New human G-protein coupled receptor X, GPCR, polypeptide useful in
 PT treatment or prevention of GPCR associated disorders e.g.
 PT cardiomyopathy or atherosclerosis, and to screen for antagonists and
 PT agonists useful therapeutically
 XX
 PS Claim 9; Page 11; 157bp; English.
 XX
 CC The invention relates to nucleic acid sequences (ABA81529-ABA81552) that
 CC encode G-coupled protein-receptor related polypeptides
 CC (ABBA4522-ABBA4543). The isolated polypeptide having a sequence differing
 CC by no more than 15 % of amino acid residues from one of 22 amino acid
 CC sequences (or mature forms of the sequences), fully defined in the
 CC specification and corresponding to human G-protein coupled receptor X
 CC (GPCR) polypeptides. The polypeptides have potential cardiant
 CC antiarteriosclerotic, anabolic, cytostratic and antiviral activity. The
 CC polypeptides can be administered therapeutically, especially using gene
 CC therapy and expressing the encoding DNA in vivo, to treat or prevent
 CC GPCR-associated disorders, especially in humans. For example, they can
 CC be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
 CC related to signal processing and metabolic pathway modulation (e.g.
 CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple

CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disorder, Huntington's disease), immune disorders,
 CC haematopoietic disorders, developmental diseases, neurological disorders,
 CC bacterial, fungal, protozoal and viral infections (e.g. with human
 CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
 CC to determine the presence of or predisposition to a disease associated
 CC with altered levels of the polypeptide in mammals (especially humans) by
 CC detecting alterations in polypeptide expression levels relative to
 CC control samples. They are useful to identify agents binding polypeptide
 CC (e.g. cellular receptors or downstream effectors) and/or agents
 CC modulating cellular polypeptide expression or activity, useful as
 CC antagonists and agonists in disease treatment.
 XX
 SQ Sequence 1104 BP; 216 A; 318 C; 295 G; 275 T; 0 other;

Query Match 91.6%; Score 1093.6; DB 22; Length 1104;
 Best Local Similarity 99.6%; Pred. No. 2.1e-297;
 Matches 1096; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	95	GTGCCATTGTGGGAGCTCCCTGGGCTGCTGCACCCGAGACCTGCTCTGCCCGCA	154
DB	1	GTGCCATTGTGGGAGCTCCCTGGGCTGCTGCACCCGAGACCTGCTCTGCCCGCA	60
QY	155	TGTACACGGGCTCGTCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCCGCGC	214
DB	61	TGTACACGGGCTCGTCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCCGCGC	120
QY	215	TGCTCATTTGGGCTTTGTGCGGCGCAGTACAGGAGTGGGCTGCTGCTGCTTCT	274
DB	121	TGCTCATTTGGGCTTTGTGCGGCGCAGTACAGGAGTGGGCTGCTGCTGCTTCT	180
QY	275	GCTTCCACATGAAGACCTGGAAGCCAGACACTGTTTACCTTTGCAATTTGGCGCTG	334
DB	181	GCTTCCACATGAAGACCTGGAAGCCAGACACTGTTTACCTTTGCAATTTGGCGCTG	240
QY	335	ATTTCCTCTTATGATCTGCTGCTTTTGGACAGACTATTTACCTAGACGTAGACT	394
DB	241	ATTTCCTCTTATGATCTGCTGCTTTTGGACAGACTATTTACCTAGACGTAGACT	300
QY	395	GGGCTTTGGGAGACATTCCTGCGAGGGGGCTTCAAGTTGGCATGAACAGGGCGG	454
DB	301	GGGCTTTGGGAGACATTCCTGCGAGGGGGCTTCAAGTTGGCATGAACAGGGCGG	360
QY	455	GGAGCATGTTCTTAAAGTGTGCTGCGAGAGATTTTCAAAAGTGTCCACCCG	514
DB	361	GGAGCATGTTCTTAAAGTGTGCTGCGAGAGATTTTCAAAAGTGTCCACCCG	420
QY	515	ACCACGCGGTGAACATATCTCCACCCGGGTGCGCTGGCATGCTGCAACCTGTGGG	574
DB	421	ACCACGCGGTGAACATATCTCCACCCGGGTGCGCTGGCATGCTGCAACCTGTGGG	480
QY	575	CCCTGTCATCTGGGAAACAGTATCTTTTGTGGAAGAACATCTGCTGGAAGAGA	634
DB	481	CCCTGTCATCTGGGAAACAGTATCTTTTGTGGAAGAACATCTGCTGGAAGAGA	540
QY	635	CGGCGCTCTCTGTGAAGCTTCAATCATGAGTCCGCAATGCTGCGACAGCATCATGT	694
DB	541	CGGCGCTCTCTGTGAAGCTTCAATCATGAGTCCGCAATGCTGCGACAGCATCATGT	600
QY	655	TCCAGCTGGAATTTCTTATGCGCTTGGCATCATTTATTTGCTCTTCAAGATTGTT	754
DB	601	TCCAGCTGGAATTTCTTATGCGCTTGGCATCATTTATTTGCTCTTCAAGATTGTT	660
QY	755	GGAGCTGAGGCGAGGACAGAGCTGCGAGACAGGCTGCGATGAAGAGAGCCGCGT	814
DB	661	GGAGCTGAGGCGAGGACAGAGCTGCGAGACAGGCTGCGATGAAGAGAGCCGCGT	720
QY	815	TCATCATGATGATGAGCAATTTGTTTCAATCATGATCTTCCAGGCTGTGCTAGAC	874
DB	721	TCATCATGATGATGAGCAATTTGTTTCAATCATGATCTTCCAGGCTGTGCTAGAC	780
QY	875	TCATTTTCTTGTGACGAGTCCCTGAGTCCGATCCCTCTGTCCATGAGGCGCTGC	934

Db	781	TCTATTTCCTGTGAGCGGTGCGCTCGAGTGCCTGCGCATCCCTCTGTCATNAGGAGGCCCTGC	840
Qy	935	ACATPACCCCTPAGGTTCACTTCACTACATGAAACAGCATGCTCGAATCCCTCGGTGATATATTTT	994
Db	841	ACATPACCCCTPAGGTTCACTTCACTACATGAAACAGCATGCTCGAATCCCTCGGTGATATATTTT	900
Qy	995	CAAGCCCTCTCTTCCCAATTTACACAAGCTCAAAATCTGCACTGGAACCAAGC	1054
Db	901	CAAGCCCTCTCTTCCCAATTTACACAAGCTCAAAATCTGCACTGGAACCAAGC	960
Qy	1055	AGCCAGGACACTCAAAAAACAAAGGCCGAGAGAGATGCCAATTTGAACTTCGATGCA	1114
Db	961	AGCCAGGACACTCAAAAAACAAAGGCCGAGAGAGATGCCAATTTGAACTTCGATGCA	1020
Qy	1115	GGAGTTGCATAGTGTGGCAATATGTTTCCAAAGCCAGTGTATGGGCAATGGATCCCC	1174
Db	1021	GGAGTTGCATAGTGTGGCAATATGTTTCCAAAGCCAGTGTATGGGCAATGGATCCCC	1080
Qy	1175	ACATGTGTAGTGGCACTGA 1194	
Db	1081	ACATGTGTAGTGGCACTGA 1100	
RESULT 5			
ID	AAD26371	standard; cDNA; 1083 BP.	
XX	AC	AAD26371;	
XX	AD	26-MAR-2002 (first entry)	
XX	DE	Human G-protein coupled receptor 3 (GCREC-3) cDNA.	
XX	KW	Human; G-protein coupled receptor 3; cell proliferative disorder;	
KW	KW	arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy;	
KW	KW	Alzheimer's disease; Parkinson's disease; cardiovascular disorder;	
KW	KW	atherosclerosis; hypertension; myocardial infarction; peptic ulcer;	
KW	KW	gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder;	
KW	KW	acquired immune deficiency syndrome; inflammatory disorder; infection	
KW	KW	Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS	
XX	OS	diabetes; obesity; osteoporosis; gene therapy; GCREC-3; ss.	
XX	OS	Homo sapiens.	
XX	XX		
XX	XX	Key	Location/Qualifiers
FT	FT	CDS	43..1083
FT	FT		/*tag= a
FT	FT		/product= "Human GCREC-3 protein"
FT	FT	sig_peptide	43..138
FT	FT		/*tag= b
FT	FT	mat_peptide	139..1080
FT	FT		/*tag= c
XX	XX		/product= "Human mature GCREC-3 protein"
XX	XX		
XX	XX	WO200187937-A2.	
XX	XX		
XX	XX	22-NOV-2001.	
XX	XX		
XX	XX	17-MAY-2001; 2001WO-US16285.	
XX	XX		
PR	PR	18-MAY-2000; 2000US-205628P.	
PR	PR	22-MAY-2000; 2000US-206222P.	
PR	PR	25-MAY-2000; 2000US-207566P.	
PR	PR	02-JUN-2000; 2000US-208834P.	
PR	PR	02-JUN-2000; 2000US-208834P.	
XX	XX		
PA	PA	(INCYTE GENOMICS INC.	
XX	XX		
PI	PI	Patterson C, Lu DM, Thornton M, Lu Y, Tribouley CM, Graul R,	
PI	PI	Khan FA, Gandhi AR, Walla NK, Nguyen DB, Yue H, Hafalia A;	
PI	PI	Elliott VS, Lal P, Reddy R, Kallick DA, Tang TY, Au-Young J;	
XX	XX		
DR	DR	WPI; 2002-089844/12.	

DR	P-PSDB:AAE16172.	
XX		
PT	Novel G-protein coupled receptors and polynucleotides useful for	
PT	diagnosis, treatment and prevention of disorders of cell proliferation,	
PT	neurological, cardiovascular, metabolic disorders and viral infections	
XX		
PS	Claim 5, Page 112; 115pp; English.	
XX		
CC	The invention relates to human G-protein coupled receptor (GPRC)	
CC	polypeptides and polynucleotides. GPRC polypeptides are useful for	
CC	screening compounds that modulate their activity. They are useful in	
CC	the diagnosis, prevention and treatment of disorders which include	
CC	cell proliferative disorders such as arteriosclerosis, hepatitis,	
CC	myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia,	
CC	lymphoma; neurological disorders such as epilepsy, ischemic	
CC	cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,	
CC	Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral	
CC	meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia;	
CC	cardiovascular disorders such as arteriovenous fistula, atherosclerosis,	
CC	hypertension, vascular tumours, myocardial infarction, hypertensive	
CC	heart disease, infective endocarditis, cardiomyopathy, myocarditis;	
CC	gastrointestinal disorders such as dysphagia, peptic oesophagitis,	
CC	emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,	
CC	constipation, acquired immune deficiency syndrome (AIDS), hepatic	
CC	encephalopathy; autoimmune/inflammatory disorders such as Addison's	
CC	disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact	
CC	dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,	
CC	erysipema, Grave's disease, gout, multiple sclerosis, rheumatoid	
CC	arthritis, systemic lupus erythematosus, uveitis, viral, bacterial,	
CC	fungal, parasitic, protozoal and helminthic infections and trauma;	
CC	metabolic disorders such as diabetes, obesity and osteoporosis; and	
CC	viral infections such as infection caused by viral agent classified as	
CC	adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention	
CC	are useful as probes for assessing toxicity of test compounds. They are	
CC	also used in gene therapy. The present sequence is human G-protein	
XX	coupled receptor 3 (GPRC-3) cDNA.	
XX		
SQ	Sequence 1083 BP; 211 A; 314 C; 288 G; 270 T; 0 other;	
	Query Match 90.4%; Score 1079.8; DB 24; Length 1083;	
	Best Local Similarity 99.8%; Pred. No. 1.6e-293;	
	Matches 1081; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	112 CCCTGGGCTGCTCTGACACCCGGACACCTGCTCTGTCCTCCCGCATGTACAGGGCTGTC 171	
DB	1 CCCTGGGCTGCTCTGACACCCGGACACCTGCTCTGTCCTCCCGCATGTACAGGGCTGTC 60	
QY	172 TGGCGATGAGAGGGGAGACCATCTCCAGAGGATGAGCCGCGCTGCTCATTTGGGCTTT 231	
DB	61 TGGCGATGAGAGGGGAGACCATCTCCAGAGGATGAGCCGCGCTGCTCATTTGGGCTTT 120	
QY	232 GTGCTGGGGCACTAGGCATGGGGGTGGCCCTGTGTGGTTTCTGCTTCACATGAAGAC 291	
DB	121 GTGCTGGGGCACTAGGCATGGGGGTGGCCCTGTGTGGTTTCTGCTTCACATGAAGAC 180	
QY	292 TGGAGCCAGACACTGTTTAACCTTTCAATTTGGCCGTGGCTGATTTCTCTTAATGATC 351	
DB	181 TGGAGCCAGACACTGTTTAACCTTTCAATTTGGCCGTGGCTGATTTCTCTTAATGATC 240	
QY	352 TGGCGGCTTTTGGACAGACATTAACCTAGAGCTAGACACTGGGCTTTTGGGAGACTT 411	
DB	241 TGGCGGCTTTTGGACAGACATTAACCTAGAGCTAGACACTGGGCTTTTGGGAGACTT 300	
QY	412 CCCTGCGAGTGGGGCTCTTCACTTTGGCCATGAACAGGGCCGGAGAGCATGTTGTTCTT 471	
DB	301 CCCTGCGAGTGGGGCTCTTCACTTTGGCCATGAACAGGGCCGGAGAGCATGTTGTTCTT 360	
QY	472 ACGGTGTGGCTTGGCAGACAGTATTTCAAGTGTTCACCCACACGCGGTGAACACT 531	
DB	361 ACGGTGTGGCTTGGCAGACAGTATTTCAAGTGTTCACCCACACGCGGTGAACACT 420	
QY	532 ATCTGCACCCGGGATGGCGGCTGGCATCGTCTGCACCTGTGTGGCCCTGTGATCTCTGGGA 591	

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Db 421 ATCTCCACCCGGGTGGCGCTGGCATGCTGACCTGTGGGCTCTGTCATCTCTGGGA 480
Oy 592 ACAGTATATCTTTTGTGGAGAACCATCTCTGCGCAAGACGGCCGCTCTCTGTAG 651
Db 481 ACAGTATATCTTTTGTGGAGAACCATCTCTGCGCAAGACGGCCGCTCTCTGTAG 540
Oy 652 AGCTTCATCATGAGTGGGCCAATGGCTGGCAAGCATCATGTTCCAGCTGGATCTTT 711
Db 541 AGCTTCATCATGAGTGGGCCAATGGCTGGCAAGCATCATGTTCCAGCTGGATCTTT 600
Oy 712 ATGCCCTTGGGATCATCTTTATTTTCTCTCTCAAGATTGTTTGAAGCTTGAAGGAG 771
Db 601 ATGCCCTTGGGATCATCTTTATTTTCTCTCTCAAGATTGTTTGAAGCTTGAAGGAG 660
Oy 772 CAGCAGCTGGCCAGACAGGCTCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 831
Db 661 CAGCAGCTGGCCAGACAGGCTCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Oy 832 ATTTGTTTCATCATGATGATCTGACCTGCGCAGCTGTCTGCTAGACTATTTCTCTGAGC 891
Db 721 ATTTGTTTCATCATGATGATCTGACCTGCGCAGCTGTCTGCTAGACTATTTCTCTGAGC 780
Oy 892 GTGCCCTCGAGTGGCTGCGCATCCCTCTGTCTCAATGGGGCCCTGCAATACCTCTGAGCTTC 951
Db 781 GTGCCCTCGAGTGGCTGCGCATCCCTCTGTCTCAATGGGGCCCTGCAATACCTCTGAGCTTC 840
Oy 952 ACCTACATGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1011
Db 841 ACCTACATGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Oy 1012 AATTTCTACACAGCTCAAAATCTGAGTCTGAGAACCCAGAGAGAGAGAGAGAGAGAGAG 1071
Db 901 AATTTCTACACAGCTCAAAATCTGAGTCTGAGAACCCAGAGAGAGAGAGAGAGAGAGAG 960
Oy 1072 ACACAAAGGCGGAGAGAGATGCCAATTTTGAACCTGCTGCGAGAGTTCAGTGTG 1131
Db 961 ACACAAAGGCGGAGAGAGATGCCAATTTTGAACCTGCTGCGAGAGTTCAGTGTG 1020
Oy 1132 GCAAAATGTTTCCAAAGCCAGTGTGATGGGCAATGGGATCCCAATTTTGAAGTGGGAC 1191
Db 1021 GCAAAATGTTTCCAAAGCCAGTGTGATGGGCAATGGGATCCCAATTTTGAAGTGGGAC 1080
Oy 1192 TGA 1194
Db 1081 TGA 1083

RESULT 6
ABA81529
ID ABA81529 standard; DNA, 1050 BP.
XX
AC ABA81529;
XX
DT 28-JAN-2002 (first entry)
XX
DE Human GPCR1a polynucleotide seq ID NO 1.
XX
KW Human; GPCR; G-coupled protein-receptor; cardiac; antiarteriosclerotic;
KW anabolic; cytosolic; antiviral; gene therapy; cardiomyopathy; obesity;
KW anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
KW asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;
KW infection; human immunodeficiency virus; HIV; de.
XX
OS Homo sapiens.
XX
PN WO200174904-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10241.
XX
PR 31-MAR-2000; 2000US-193664P.

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PR 05-APR-2000; 2000US-194614P.
PR 06-APR-2000; 2000US-195063P.
PR 06-APR-2000; 2000US-195066P.
PR 06-APR-2000; 2000US-195067P.
PR 06-APR-2000; 2000US-195068P.
PR 06-APR-2000; 2000US-195069P.
PR 06-APR-2000; 2000US-195070P.
PR 06-APR-2000; 2000US-19510P.
PR 06-APR-2000; 2000US-219855P.
PR 27-JUL-2000; 2000US-221284P.
PR 28-JUL-2000; 2000US-221325P.
PR 11-AUG-2000; 2000US-224588P.
PR 11-OCT-2000; 2000US-239613P.
PR 18-JAN-2001; 2001US-262508P.
PR 23-JAN-2001; 2001US-263433P.
PR 23-JAN-2001; 2001US-263604P.
PR 30-JAN-2001; 2001US-265161P.
PR 29-MAR-2001; 2001US-0823172.

XX
XX (CURA-) CURAGEN CORP.
XX
XX Majumder K, Vernet CM, Casman SJ, Wolenc AR, Spaderma SK,
XX Padigaru M, Mishu VS, Tcheuher VT, Spytek KA, Li L,
XX Baumgartner JC, Gusev VY;
XX
XX WPI; 2001-639351/73.
XX P-FSD; ABA84522.
XX
XX New human G-protein coupled receptor X, GPCR, polypeptide useful in
XX treatment or prevention of GPCR associated disorders e.g.
XX cardiomyopathy or atherosclerosis, and to screen for antagonists and
XX agonists useful therapeutically
XX
XX Claim 9; Page 7; 157pp; English.
XX
XX The invention relates to nucleic acid sequences (ABA81529-ABA81552) that
XX encode G-coupled protein-receptor related polypeptides
XX (ABA84522-ABA84543). The isolated polypeptide having a sequence differing
XX by no more than 15 % of amino acid residues from one of 22 amino acid
XX sequences (or mature forms of the sequences), fully defined in the
XX specification and corresponding to human G-protein coupled receptor X
XX (GPCR) polypeptides. The polypeptides have potential cardiac,
XX antiarteriosclerotic, anabolic, cytosolic and antiviral activity. The
XX polypeptides can be administered therapeutically, especially using gene
XX therapy and expressing the encoding DNA in vivo, to treat or prevent
XX GPCR-associated disorders, especially in humans. For example, they can
XX be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
XX related to signal processing and metabolic pathway modulation (e.g.
XX obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
XX sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
XX disease, Parkinson's disorder, Huntington's disease), immune disorders,
XX haematopoietic disorders, developmental diseases, neurological disorders,
XX bacterial, fungal, protozoal and viral infections (e.g. with human
XX immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
XX to determine the presence of or predisposition to a disease associated
XX with altered levels of the polypeptide in mammals (especially humans) by
XX detecting alterations in polypeptide expression levels relative to
XX control samples. They are useful to identify agents binding polypeptide
XX (e.g. cellular receptors or downstream effectors) and/or agents
XX modulating cellular polypeptide expression or activity, useful as
XX antagonists and agonists in disease treatment.
XX
XX Sequence 1050 BP; 211 A; 299 C; 279 G; 261 T; 0 other;
XX
XX Query Match 87.5%; Score 1044.4; DB 22; Length 1050;
XX Best Local Similarity 99.9%; Pred. No. 1.5e-283;
XX Matches 1045; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 149 CGCCATGATCAACAGGAGTGGCTGCGCATCGAGGAGGACACATCTCCAGATGATGC 208
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Db 61 CGCCGCTGCTATTTGGCTTTTGTCTGCGCACTAGGCAATGGGCTGCTGTGTG 120
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Qy 329 TGGCTGATTTCTCTTATGATTCGCTGCTTTTGGAGAGACTATTTACCTCAGAGCTA 388
Db 181 TGGCTGATTTCTCTTATGATTCGCTGCTTTTGGAGAGACTATTTACCTCAGAGCTA 240
Qy 389 GACACTGGGCTTTTGGGGAACATTCCTGCGAGTGGGGCTCTTACGCTTGGCAATGAACA 448
Db 241 GACACTGGGCTTTTGGGGAACATTCCTGCGAGTGGGGCTCTTACGCTTGGCAATGAACA 300
Qy 449 GGGCCGGAGAGCATGTTCTTACGGTGTGCTGCGAGAGGATTTTCAAAAGTGTCC 508
Db 301 GGGCCGGAGAGCATGTTCTTACGGTGTGCTGCGAGAGGATTTTCAAAAGTGTCC 360
Qy 509 ACCCCCAACAGCGCGGTGAACATATCTTCCACCCGGGTGGGGCTGGCATGTCTGACCC 568
Db 361 ACCCCCAACAGCGCGGTGAACATATCTTCCACCCGGGTGGGGCTGGCATGTCTGACCC 420
Qy 569 TGTGGGCGCTGTGATCTCTGGAACAGGTATCTTTTGTGGAAGAACATCTCGGTGTC 628
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Db 541 TCATGTTCCAGCTGGAATCTTTATGCCCCCTGGGCATCATTTATTTGCTCTTCAAGA 600
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Qy 869 CTAGACTTATTTCTCTGAGCGGTGCTGAGAGTGTCCGATCCCTGTCTGATGGG 928
Db 721 CTAGACTTATTTCTCTGAGCGGTGCTGAGAGTGTCCGATCCCTGTCTGATGGG 780
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Db 1021 ATCCCAATTTGTTGATGGCACTGA 1046

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XX 28-JAN-2002 (first entry)
DT Human GPCR1b polynucleotide SEQ ID NO 3.
XX
DE Human, GPCR, G-coupled protein-receptor; cardiac; antiarteriosclerotic;
XX anabolic; cytoskeletal; antiviral; gene therapy; cardiomyopathy; obesity;
XX anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
XX asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;
XX infection; human immunodeficiency virus; HIV; ds.
XX
OS Homo sapiens.
XX
PN WO200174904-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US10241.
XX
XX 31-MAR-2000; 2000US-19364P.
PR 05-APR-2000; 2000US-194614P.
PR 06-APR-2000; 2000US-195063P.
PR 06-APR-2000; 2000US-195066P.
PR 06-APR-2000; 2000US-195067P.
PR 06-APR-2000; 2000US-195068P.
PR 06-APR-2000; 2000US-195069P.
PR 06-APR-2000; 2000US-19510P.
PR 21-JUL-2000; 2000US-219855P.
PR 27-JUL-2000; 2000US-221284P.
PR 28-JUL-2000; 2000US-221325P.
PR 11-AUG-2000; 2000US-224588P.
PR 11-OCT-2000; 2000US-239613P.
PR 18-JAN-2001; 2001US-262508P.
PR 23-JAN-2001; 2001US-263433P.
PR 23-JAN-2001; 2001US-263604P.
PR 30-JAN-2001; 2001US-265161P.
PR 29-MAR-2001; 2001US-0823172.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Majumder K, Vernet CM, Caeman SJ, Wolenc AR, Spaderna SK,
PI Padigaru M, Mishra VS, Tchervet VT, Spytek KA, Li L,
PI Baumgartner JC, Gusev VY.
XX
XX MPI: 2001-639351/73.
XX
XX P-PSDB: ABB44522.
XX
XX New human G-protein coupled receptor X, GPCR, polypeptide useful in
XX treatment or prevention of GPCR associated disorders e.g.
XX cardiomyopathy or atherosclerosis, and to screen for antagonists and
XX agonists useful therapeutically.
XX
XX Claim 9; Page 10; 157pp; English.
XX
XX The invention relates to nucleic acid sequences (ABA81529-ABA81552) that
XX encode G-coupled protein-receptor related polypeptides
XX (ABA44522-ABA44543). The isolated polypeptide having a sequence differing
XX by no more than 15 % of amino acid residues from one of 22 amino acid
XX sequences (or mature forms of the sequences), fully defined in the
XX specification and corresponding to human G-protein coupled receptor X
XX (GPCR) polypeptides. The polypeptides have potential cardiac,
XX antiarteriosclerotic, anabolic, cytoskeletal and antiviral activity.
XX polypeptides can be administered therapeutically, especially using gene
XX therapy and expressing the encoding DNA in vivo, to treat or prevent
XX GPCR-associated disorders, especially in humans. For example, they can
XX be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
XX related to signal processing and metabolic pathway modulation (e.g.
XX obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
XX sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
XX disease, Parkinson's disorder, Huntington's disease), immune disorders,
XX hematopoietic disorders, developmental diseases, neurological disorders,
XX bacterial, fungal, protozoal and viral infections (e.g. with human

```


CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
CC to determine the presence of or predisposition to a disease associated
CC with altered levels of the polypeptide in mammals (especially humans) by
CC detecting alterations in polypeptide expression levels relative to
CC control samples. They are useful to identify agents binding polypeptide
CC (e.g. cellular receptors or downstream effectors) and/or agents
CC modulating cellular polypeptide expression or activity, useful as
CC antagonists and agonists in disease treatment.

XX Sequence 1050 BP; 211 A; 298 C; 279 G; 262 T; 0 other;

Query Match 87.4%; Score 1043.4; DB 22; Length 1050;
Best Local Similarity 99.9%; Pred. No. 2.8e-283;
Matches 1044; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 150 CGCATGTAACAAGGCTGCTGCTGCGCATCGAGGGGACACACCATCCAGATGATGCC 209
DB 2 CGCATGTAACAAGGCTGCTGCTGCGCATCGAGGGGACACACCATCCAGATGATGCC 61
QY 210 GCCGCTGCTCATTTGTCCTTTGCTGGGCGCATAGGCAATGGGCTGCTGCTG 269
DB 62 GCCGCTGCTCATTTGTCCTTTGCTGGGCGCATAGGCAATGGGCTGCTGCTG 121
QY 270 TTTCTGCTTCCATGATAAAGCCCTGGAAGCCGACATGTTTACCTTTCAATTTGGCCGT 329
DB 122 TTTCTGCTTCCATGATAAAGCCCTGGAAGCCGACATGTTTACCTTTCAATTTGGCCGT 181
QY 330 GGGTGATTTCCCTCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 389
DB 182 GGGTGATTTCCCTCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
QY 390 ACACTGGGCTTTTGGGAGACATTCCTGCGAGTGGGCTCTTACGCTTGGGCGCATGAAC 449
DB 242 ACACTGGGCTTTTGGGAGACATTCCTGCGAGTGGGCTCTTACGCTTGGGCGCATGAAC 301
QY 450 GGGCGGAGCATGCTGCTTCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 509
DB 302 GGGCGGAGCATGCTGCTTCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
QY 510 CCCCACCAAGCGGCTGGAACATCTCCACCCGAGTGGGCTGGGCGCATGCTGCGACCT 569
DB 362 CCCCACCAAGCGGCTGGAACATCTCCACCCGAGTGGGCTGGGCGCATGCTGCGACCT 421
QY 570 GTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
DB 422 GTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 481
QY 630 AGAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 689
DB 482 AGAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 541
QY 690 CATGTTCCAGCTGAGGCTTCTTATGCGCCCTCGGACATCTTATTTTGTCTCCCTCAAGT 749
DB 542 CATGTTCCAGCTGAGGCTTCTTATGCGCCCTCGGACATCTTATTTTGTCTCCCTCAAGT 601
QY 750 TGTGTTGAGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 809
DB 602 TGTGTTGAGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 661
QY 810 CCGGTTTCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 869
DB 662 CCGGTTTCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 721
QY 870 TAGACTTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 929
DB 722 TAGACTTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
QY 930 CCGTGAATTAACCTGAGCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 989
DB 782 CCGTGAATTAACCTGAGCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 841
QY 990 TTTTTCAGGCGCTCTTTTCCCAATTTCAACAAGCTCAAAATTTGAGTGTGAAC 1049

DB 842 TTTTTCAGGCGCTCTTTTCCCAATTTCAACAAGCTCAAAATTTGAGTGTGAAC 901
QY 1050 CAAGCAGCCAGACACTCAAAAACACAAAGCCGGAAGAGATGCCAATTTGAACTCGG 1109
DB 902 CAAGCAGCCAGACACTCAAAAACACAAAGCCGGAAGAGATGCCAATTTGAACTCGG 961
QY 1110 TCGCAGAGGTTGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1169
DB 962 TCGCAGAGGTTGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1021
QY 1170 TCCGACATTTGAGGAGGACCTGA 1194
DB 1022 TCCGACATTTGAGGAGGACCTGA 1046

RESULT 8
AAS12581
ID AAS12581 standard; cDNA; 1041 BP.
XX
AC AAS12581;
XX
DT 19-DEC-2001 (first entry)
XX
DE cDNA encoding novel human G protein-coupled receptor (GPCR).
XX
KW Human; G-protein coupled receptor; GPCR; chemokine receptor; protease;
KW hyperproliferative disorder; neurological disorder; psychiatric disease;
KW inflammatory disorder; respiratory disorder; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1041
FT /*tag= a
FT /product= "GPCR protein"
XX
EN W0200173029-A2.
XX
PD 04-OCT-2001.
XX
PE 27-MAR-2001; 2001MO-US09522.
XX
PR 27-MAR-2000; 2000US-192419P.
PR 06-SEP-2000; 2000US-230459P.
PR 20-SEP-2000; 2000US-066535.
XX
PA (PEKE) PE CORP NY.
XX
PI Ye J, Cravchik A, Di Francesco V, Beasley EM;
XX
DR WPI; 2001-616503/71.
DR P-PSDB; AAU06197.
XX
FT Novel human G-protein coupled receptor proteins and nucleic acid
FT molecules encoding the protein for use in developing human therapeutics
FT and diagnostic compositions and for identifying modulators of the
FT protein
XX
PS Claim 23; Fig 1; 66pp; English.
XX
XX The present invention relates to the isolation of a novel human G-protein
XX coupled receptor (GPCR) which is related to the chemokine receptor
XX subfamily. The cDNA and gene sequences encoding for GPCR are also
XX given in the invention. The sequences of the invention are useful
XX for diagnosing and treating diseases or conditions mediated by human
XX processes. Such diseases include hyperproliferative disorders
XX (e.g. hyperplasia), neurological disorders (e.g. Parkinson's disease),
XX psychiatric diseases (e.g. schizophrenia), inflammatory disorders
XX (e.g. diabetes) and respiratory disorders (e.g. adult respiratory
XX distress syndrome, ARDS). The GPCR protein is also useful for identifying
XX a modulator of the expression of the protein. It also serves as a target
XX for identifying agents for use in mammalian therapeutic applications,
XX e.g. a human drug, particularly modulating a biological or pathological

CC response in a cell or tissue that expresses the protein, in biological
 CC assays related to GPCRs that are related to members of the chemokine
 CC receptor subfamily, in drug screening assays and in competition binding
 CC assays. GPCR is also useful in diagnosing a disease or predisposition to
 CC a disease mediated by the peptide, in pharmacogenomic analysis. The
 CC polynucleotide sequences can also be used in gene therapy. The present
 CC sequence encodes for the novel human GPCR of the invention.

XX Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 other;

Query Match 87.1%; Score 1039.4; DB 22; Length 1041;
 Best Local Similarity 99.9%; Pred. No. 3,7e-282;
 Matches 1040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 154 ATGACAAACGGGTGCTGCTGCGCATGAGAGGAGACACATCTCCAGATGCCCGG 213
 DB 1 ATGACAAACGGGTGCTGCTGCGCATGAGAGGAGACACATCTCCAGATGCCCGG 60
 QY 214 CTGCTCATTTGGGCTTTGGTGGGCGCATAGGCAATGGGGTGGCTGTGGTTC 273
 DB 61 CTGCTCATTTGGGCTTTGGTGGGCGCATAGGCAATGGGGTGGCTGTGGTTC 120
 QY 274 TGCTTCCACATGAGACCTGGAAGCCAGACACTTTTCACTTTTGGCGGTGGCT 333
 DB 121 TGCTTCCACATGAGACCTGGAAGCCAGACACTTTTCACTTTTGGCGGTGGCT 180
 QY 334 GATTTCCTCTTATGATCTGCTGCTGCTTTTGGACAGACTATTACTCAGACCTAGACAC 393
 DB 181 GATTTCCTCTTATGATCTGCTGCTGCTTTTGGACAGACTATTACTCAGACCTAGACAC 240
 QY 394 TGGGCTTTTGGGAGCATTTCCCTGCGAGTGGGGCTCTTCACTTTGGCGCATGAACAGGGCC 453
 DB 241 TGGGCTTTTGGGAGCATTTCCCTGCGAGTGGGGCTCTTCACTTTGGCGCATGAACAGGGCC 300
 QY 454 GGGAGCATCGTGTCTCTTAAGTGTGTGGTGGCGACAGATTTTCAAGAGTGTCCACCC 513
 DB 301 GGGAGCATCGTGTCTCTTAAGTGTGTGGTGGCGACAGATTTTCAAGAGTGTCCACCC 360
 QY 514 CACACGCGGTGAACATCTATCTCCACCGGGTGGCGCTGGCATCGTCTGACCTGTGG 573
 DB 361 CACACGCGGTGAACATCTATCTCCACCGGGTGGCGCTGGCATCGTCTGACCTGTGG 420
 QY 574 GCCCTGATCATCTGGGAACAGTGTATCTTTTGTGGAGAACCATCTCTGCGTGAAG 633
 DB 421 GCCCTGATCATCTGGGAACAGTGTATCTTTTGTGGAGAACCATCTCTGCGTGAAG 480
 QY 634 ACCGCTCTCTCTGTGAGACTTCATATGAGTGTGGCCATAGTGTGGACGACATCATG 693
 DB 481 ACCGCTCTCTCTGTGAGACTTCATATGAGTGTGGCCATAGTGTGGACGACATCATG 540
 QY 694 TTCCAGCTGAGATCTTTATGCCCCCTCGGACATCTTATTTTGTCTCTCAAGATTGTT 753
 DB 541 TTCCAGCTGAGATCTTTATGCCCCCTCGGACATCTTATTTTGTCTCTCAAGATTGTT 600
 QY 754 TGAAGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 813
 DB 601 TGAAGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
 QY 814 TTATCATGTGTGTGGGAATTTGTGTATATCATATGCTACTGCTGCTGTCTGTAGA 873
 DB 661 TTATCATGTGTGTGGGAATTTGTGTATATCATATGCTACTGCTGCTGTCTGTAGA 720
 QY 874 CTATATTCTCTGAGAGGTGCTGCTGAGTGGCTGAGATCCCTCTGTGCTATGAGGCGCTG 933
 DB 721 CTATATTCTCTGAGAGGTGCTGCTGAGTGGCTGAGATCCCTCTGTGCTATGAGGCGCTG 780
 QY 934 CACATAACCTCTGAGCTTACCTACATGAGAGAGATGTGATCCCTGTGTATATTTT 993
 DB 781 CACATAACCTCTGAGCTTACCTACATGAGAGAGATGTGATCCCTGTGTATATTTT 840
 QY 994 TCAAGCCCTCTCTTCCCAATTTCTACAAAGCTCAAAATCTGCAAGTGTGAAACCCAG 1053
 DB 841 TCAAGCCCTCTCTTCCCAATTTCTACAAAGCTCAAAATCTGCAAGTGTGAAACCCAG 900

QY 1054 CAGCAGGACACTCAAAAACAAAGGCGGAGAGATGCCAATTTTGAACCTTGGTGC 1113
 DB 901 CAGCAGGACACTCAAAAACAAAGGCGGAGAGATGCCAATTTTGAACCTTGGTGC 960
 QY 1114 AGGAGTTCATCATGCTGTGGCAATATGTTTCCAAAGCCAGTGTGATGGGCAATGGATCCC 1173
 DB 961 AGGAGTTCATCATGCTGTGGCAATATGTTTCCAAAGCCAGTGTGATGGGCAATGGATCCC 1020
 QY 1174 CACATTTGTGATGGCACTGA 1194
 DB 1021 CACATTTGTGATGGCACTGA 1041

RESULT 9
 ID AAS07946
 XX AAS07946 standard; cDNA; 1041 BP.
 AC AAS07946;
 XX
 DT 23-OCT-2001 (first entry)
 XX
 DE Human cDNA encoding G-protein coupled receptor, hrup19.
 KW Human; G-protein coupled receptor; GPCR; hrup19; agonist;
 KW inverse agonist; lung cancer; ss.
 XX OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..1041
 FT CDS /*tag= a
 FT /product= "hrup19"
 XX
 EN WO200136471-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000; 2000WO-US31509.
 XX
 PR 17-NOV-1999; 99US-0166088.
 PR 17-NOV-1999; 99US-0166099.
 PR 17-NOV-1999; 99US-0166369.
 PR 23-DEC-1999; 99US-0171900.
 PR 23-DEC-1999; 99US-0171901.
 PR 23-DEC-1999; 99US-0171902.
 PR 11-FEB-2000; 2000US-0181749.
 PR 14-MAR-2000; 2000US-0189258.
 PR 14-MAR-2000; 2000US-0189259.
 PR 10-APR-2000; 2000US-0195898.
 PR 10-APR-2000; 2000US-0195899.
 PR 10-APR-2000; 2000US-0196078.
 PR 28-APR-2000; 2000US-0200419.
 PR 12-MAY-2000; 2000US-0203630.
 PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Chen R, Dang HT, Lowitz KP;
 XX
 DR WPI; 2001-355616/37.
 DR P-PSDB; AAU04373.
 XX
 PT Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -

PS Claim 47; Page 110; 159pp; English.

XX The sequence encodes a human G-protein coupled receptor (GPCR),
 CC hRPP19. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists.
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system, incorporating GPCRs can be
 CC utilized to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.

XX
 XX Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 other;
 SO
 Query Match 87.1%; Score 1039.4; DB 22; Length 1041;
 Best Local Similarity 99.9%; Pred. No. 3.7e-282;
 Matches 1040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 154 ATGTACAAAGGGTCTGCTGCTGCGCATCGAAGGGGACACCATCTCCAGGTATGCCCG 213
 Db 1 ATGTACAAAGGGTCTGCTGCTGCGCATCGAAGGGGACACCATCTCCAGGTATGCCCG 60

QY 214 CTGCTCATTTGGGCTTTGCTGGGGCGCACTAGGCAATGGGCTGCGCTGCTGCTTTC 273
 Db 61 CTGCTCATTTGGGCTTTGCTGGGGCGCACTAGGCAATGGGCTGCGCTGCTGCTTTC 120

QY 274 TGCTTCCACATGAAGACCTGGAAGCCAGCACTGTTTACCTTTTCAATTTGGCGTGGCT 333
 Db 121 TGCTTCCACATGAAGACCTGGAAGCCAGCACTGTTTACCTTTTCAATTTGGCGTGGCT 180

QY 334 GATTTCTCTTATGATGATGCTGCTGCTTTTGGAGACATATTTACCTGAGAGTACAC 393
 Db 181 GATTTCTCTTATGATGATGCTGCTGCTTTTGGAGACATATTTACCTGAGAGTACAC 240

QY 394 TGGGCTTTTGGGAGATTTCCCTGCGAGTGGGGCTTTCAAGTTGGCCATGAACAGGGCC 453
 Db 241 TGGGCTTTTGGGAGATTTCCCTGCGAGTGGGGCTTTCAAGTTGGCCATGAACAGGGCC 300

QY 454 GGGAGCATGCTGTTCTTACAGGTGGTGGCGAGAGATTTCAAGTGGTCCACCCC 513
 Db 301 GGGAGCATGCTGTTCTTACAGGTGGTGGCGAGAGATTTCAAGTGGTCCACCCC 360

QY 514 CACCAAGCGGTGAACATATCTCCACCGGGTGGCGCTGCGATGCTGACCCCTGTGG 573
 Db 361 CACCAAGCGGTGAACATATCTCCACCGGGTGGCGCTGCGATGCTGACCCCTGTGG 420

QY 574 GCGCTGCTCATCTCTGGGAACAGTATCTTTTGTGGAGAACATCTCTGCTGGAAGAG 633
 Db 421 GCGCTGCTCATCTCTGGGAACAGTATCTTTTGTGGAGAACATCTCTGCTGGAAGAG 480

QY 634 AGGCGCGTCTCTGAGAGCTTTCATGAGTGGGCAATGGCTGGGACAGCATCATG 693
 Db 481 AGGCGCGTCTCTGAGAGCTTTCATGAGTGGGCAATGGCTGGGACAGCATCATG 540

QY 694 TTCCAGCTGAGAGTCTTATATGCCCTCGGCATCATTTATTTTGTCTCTTCAAGATTGT 753
 Db 541 TTCCAGCTGAGAGTCTTATATGCCCTCGGCATCATTTATTTTGTCTCTTCAAGATTGT 600

QY 754 TGGAGCTTGAAGCGGAGGAGAGAGCTGGGCGAGAGGCTGGATGAAGAAGCGACCGG 813
 Db 601 TGGAGCTTGAAGCGGAGGAGAGAGCTGGGCGAGAGGCTGGATGAAGAAGCGACCGG 660

QY 814 TTTCATCATGATGAGTGAATTTGTTCATCATGATGAGTGGGCTGCTGCTGCTGCTGCTG 873
 Db 661 TTTCATCATGATGAGTGAATTTGTTCATCATGATGAGTGGGCTGCTGCTGCTGCTGCTG 720

QY 874 CTCTATTTCTCTGAGAGGCTGCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 933
 Db 721 CTCTATTTCTCTGAGAGGCTGCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

QY 934 CACATTAACCTTCAAGTTCATCTACATGAACAGAGTGGTGGTGGTGGTGGTGGTGGTGG 993

Db 781 CACATTAACCTTCAAGTTCATCTACATGAACAGAGTGGTGGTGGTGGTGGTGGTGGTGG 840

QY 994 TCAAGCCCTCTCTTTCCAAATTTTACAAAGCTTCAAAATGTGAGTGAACCCAG 1053
 Db 841 TCAAGCCCTCTCTTTCCAAATTTTACAAAGCTTCAAAATGTGAGTGAACCCAG 900

QY 1054 CAGCCAGGACACTCAAAACACAAAGCCGGAAGAGATGCCAATTTCCAACTCGGTGCG 1113
 Db 901 CAGCCAGGACACTCAAAACACAAAGCCGGAAGAGATGCCAATTTCCAACTCGGTGCG 960

QY 1114 AGGAGTTGATCAGTGTGGCAATAGTTTCCAAAGCAGTCTGATGGGCAATGGATCCC 1173
 Db 961 AGGAGTTGATCAGTGTGGCAATAGTTTCCAAAGCAGTCTGATGGGCAATGGATCCC 1020

QY 1174 CACATTTGATGAGTGGCCTGA 1194
 Db 1021 CACATTTGATGAGTGGCCTGA 1041

RESULT 10
 AAH51008
 ID AAH51008 standard; DNA; 1041 BP.
 XX
 AC AAH51008;
 XX
 DT 28-AUG-2001 (first entry)
 XX
 DE Human nGPCR1 coding sequence #2.
 XX
 KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;
 KW signal transduction; schizophrenia; thyroid disorder; renal failure;
 KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
 KW cardiovascular disease; proliferative disorder; hormonal disorder;
 KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 KW attention deficit-hyperactivity disorder/attention deficit disorder;
 KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
 KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 KW neuroprotective; ds.
 XX
 OS Homo sapiens.
 XX
 PN MO200136473-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000; 2000MO-US31581.
 XX
 PR 16-NOV-1999; 99US-0165838.
 PR 17-NOV-1999; 99US-0166071.
 PR 19-NOV-1999; 99US-0166678.
 PR 28-DEC-1999; 99US-0173396.
 PR 22-FEB-2000; 2000US-0184129.
 PR 28-FEB-2000; 2000US-0185421.
 PR 28-FEB-2000; 2000US-0185554.
 PR 02-MAR-2000; 2000US-0186530.
 PR 03-MAR-2000; 2000US-0186811.
 PR 09-MAR-2000; 2000US-0188114.
 PR 17-MAR-2000; 2000US-0190310.
 PR 21-MAR-2000; 2000US-0190800.
 PR 20-APR-2000; 2000US-0198568.
 PR 02-MAY-2000; 2000US-0201190.
 PR 08-MAY-2000; 2000US-0203111.
 PR 25-MAY-2000; 2000US-0207094.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Vogeli G, Wood LS, Parodi LA, Hiesch RR, Lind P, Slightom J,
 PI Schellin KA, Kayes PS, Bannigan CM, Ruff V, Sejlitz T, Ruff RM;
 DR WPI; 2001-389826/41.
 DR P-PSDB; AAG80968.
 XX
 PT New G protein-coupled receptor (nGPCR-x) and its encoding

polynucleotide useful for diagnosing and treating e.g. schizophrenia -
 Claim 4; Page 89; 261pp; English.

The present invention relates to novel G protein-coupled receptors (GPCRs) where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is the coding sequence for one such G protein-coupled receptor. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCR coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRs are useful for identifying compounds useful for treating schizophrenia. Detection of nGPCRs in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCR activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.

Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 other;

Query Match 87.1%; Score 1039.4; DB 22; Length 1041;
 Best Local Similarity 99.9%; Pred. No. 3.7e-282;
 Matches 1040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

154 ATGTACACGGGTGCTGCTGCTCCGATCGAGGGGAGACACATCTCCAGATGATGCGCG 213
 Db 1 ATGTACACGGGTGCTGCTGCTCCGATCGAGGGGAGACACATCTCCAGATGATGCGCG 60
 214 CTGCTCATTTGTCCTTTGCTGTCGGGCGCACTAGGCAATGGGCTGCTGTGTTTC 273
 Db 61 CTGCTCATTTGTCCTTTGCTGTCGGGCGCACTAGGCAATGGGCTGCTGTGTTTC 120
 274 TGGTTCACATGAAAGCTGGAGCCGAGACATCTTTTCAATTTGGCGGTGCT 333
 Db 121 TGGTTCACATGAAAGCTGGAGCCGAGACATCTTTTCAATTTGGCGGTGCT 180
 334 GATTTCTCTTATGATCTGCTGCTTTTGGAGACACTATTACCTCAGACGTAGACAC 393
 Db 181 GATTTCTCTTATGATCTGCTGCTTTTGGAGACACTATTACCTCAGACGTAGACAC 240
 394 TGGGCTTTTGGGACATTCCTGCGGAGTGGGCTCTTCACTGTTGGCCATGAAACAGGCGC 453
 Db 241 TGGGCTTTTGGGACATTCCTGCGGAGTGGGCTCTTCACTGTTGGCCATGAAACAGGCGC 300
 454 GGGAGATGCTGTTCTTACGTTGCTGCTGCGGAGACAGTATTCAAGTGTCCACCCC 513
 Db 301 GGGAGATGCTGTTCTTACGTTGCTGCTGCGGAGACAGTATTCAAGTGTCCACCCC 360
 514 CACCAAGCGGTGAACACTATCTCACCCGGGTGGCGGCTGATCTGTCACCTCTGTGG 573
 Db 361 CACCAAGCGGTGAACACTATCTCACCCGGGTGGCGGCTGATCTGTCACCTCTGTGG 420
 574 GCCCTGCTGATCTCTGGGAAACAGTATCTTTTCTGAGAAACATCTCTGCTGCAAGAG 633
 Db 421 GCCCTGCTGATCTCTGGGAAACAGTATCTTTTCTGAGAAACATCTCTGCTGCAAGAG 480
 634 AGGCGGCTCTCTGAGAGCTTCATCAGAGATTCGGCCAAATGGCTGGACGACATCAG 693
 Db 481 AGGCGGCTCTCTGAGAGCTTCATCAGAGATTCGGCCAAATGGCTGGACGACATCAG 540
 694 TTCCAGCTGAGTCTTTATGCCCCCTCGGATCATCTTATTTTGTCTTCAAGATTGTT 753
 Db 541 TTCCAGCTGAGTCTTTATGCCCCCTCGGATCATCTTATTTTGTCTTCAAGATTGTT 600
 754 TGGAGCTTGAAGCGGAGGACAGAGCTGGCCAGACAGCTCGATGAAAGAGGCGACCCGG 813

601 TGGAGCTTGAAGCGGAGGACAGAGCTGGCCAGACAGGCTCGATGAAAGAGGCGACCCGG 660
 814 TTTCATCATGATGATGGCAATTTGTTTATCATCATAGTACTCTCCGAGCGTGTCTGTAGA 873
 Db 661 TTTCATCATGATGATGGCAATTTGTTTATCATCATAGTACTCTCCGAGCGTGTCTGTAGA 720
 874 CTCTATTTCTCTGAGCGGTGCTGCTGAGTGCCTGCTGATCCCTGTGATGAGGCGCTG 933
 Db 721 CTCTATTTCTCTGAGCGGTGCTGCTGAGTGCCTGCTGATCCCTGTGATGAGGCGCTG 780
 934 CACATACCTTCAGCTTCACTCATGAAACAGATGCTGATCCCTGTGATGATTTT 993
 Db 781 CACATACCTTCAGCTTCACTCATGAAACAGATGCTGATCCCTGTGATGATTTT 840
 994 TCAAGCCCTCTCTTCCCAATTTTCAACAGCTGATGCTGATGCTGATGCTGATGCTG 1053
 Db 841 TCAAGCCCTCTCTTCCCAATTTTCAACAGCTGATGCTGATGCTGATGCTGATGCTG 900
 1054 CAGCCAGACACTCAAAAACACAAAGCGGAGAGATGCCAATTTGAACTCGGTGCG 1113
 Db 901 CAGCCAGACACTCAAAAACACAAAGCGGAGAGATGCCAATTTGAACTCGGTGCG 960
 1114 AGAGTTGCATGATGTCGCAAAATGTTTCCAAAGCCAGTCTGATGGCAATGGATCCC 1173
 Db 961 AGAGTTGCATGATGTCGCAAAATGTTTCCAAAGCCAGTCTGATGGCAATGGATCCC 1020
 1174 CACATTTGAGTGGCAGCTGA 1194
 Db 1021 CACATTTGAGTGGCAGCTGA 1041

RESULT 11
 AAL42499
 ID AAL42499 standard; DNA, 1041 BP.
 AC AAL42499;
 XX
 DT 28-JUN-2002 (first entry)
 XX
 DE Human purinergic-1-like G-protein coupled receptor (AXOR87) DNA sequence.
 XX
 KW Human; gene; ds; purinergic-1-like G-protein coupled receptor; AXOR87;
 KW immunity; autoimmunity; inflammation; immunodeficiency;
 KW bacterial infection; fungal infection; viral infection;
 KW protozoa infection; cancer; diabetes; obesity; anorexia; bulimia; asthma;
 KW psoriasis; rheumatoid arthritis; osteoarthritis; psychotic disorder;
 KW neurological disorder; vaccine; chromosome 12q24.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..1041
 FT /tag= a
 FT /product= "Human purinergic-1-like G-protein coupled
 FT receptor AXOR87"
 PN GB2365868-A.
 XX
 PD 27-FEB-2002.
 XX
 PF 25-MAY-2001; 2001GB-0012860.
 XX
 PR 30-MAY-2000; 2000US-0580675.
 PR 02-NOV-2000; 2000GB-0026839.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Ignar DM, Elshourbagy N, Gattu M, Shabon U,
 XX WPI, 2002-364852/40.

DR P-PSDB; AA014788.
 XX New purine-like G-protein coupled receptor AXOR87 polypeptide and
 PT polymorphic, useful for treating diseases related to autoimmunity,
 PT inflammation, immunodeficiency, or bacterial, fungal, viral and
 PT protozoal infections
 XX
 XX Claim 5; Page 36; 47pp; English.
 XX
 CC The invention comprises the amino acid and coding sequence of the human
 CC purine-like G-protein coupled receptor AXOR87. The AXOR87 DNA and
 CC protein sequences of the invention may be used for treating diseases
 CC related to immunity, autoimmunity, inflammation, immunodeficiency, and
 CC infections (i.e. bacterial, fungal, viral, protozoan). The AXOR87 DNA and
 CC protein sequences are particularly useful for treating: cancers,
 CC diabetes, obesity, anorexia, bulimia, asthma, psoriasis, rheumatoid
 CC arthritis, osteoarthritis, as well as psychotic and neurological
 CC disorders. The AXOR87 DNA and protein sequences may also be used as
 CC vaccines. The present DNA sequence (located on chromosome 12q24) encodes
 CC the human AXOR87 protein.
 CC
 XX
 XX

Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 other;

Query Match 87.1%; Score 1039.4; DB 24; Length 1041;
 Best Local Similarity 99.9%; Pred. No. 3.7e-282;
 Matches 1040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 154 ATGTACAAAGGGGCTGCTGCGCATCGAGGGGAGACCATCTCCAGGTGATGCGCGC 213
 DB 1 ATGTACAAAGGGGCTGCTGCGCATCGAGGGGAGACCATCTCCAGGTGATGCGCGC 60
 QY 214 CTGCTCATTTGAGCCCTTTGCTGCGGCGCATAGGCAATGAGGCTGCTGCTGCTTTC 273
 DB 61 CTGCTCATTTGAGCCCTTTGCTGCGGCGCATAGGCAATGAGGCTGCTGCTGCTTTC 120
 QY 274 TCGTTCACATGAAAGCCTGGAAGCCAGACCTGTTTACCTTTTCAATTTGGCCGTGCT 333
 DB 121 TCGTTCACATGAAAGCCTGGAAGCCAGACCTGTTTACCTTTTCAATTTGGCCGTGCT 180
 QY 334 GATTTCCCTTATGATGCTGCGCCTTTTGGAGACATATTTACCTGAGATGAGAC 393
 DB 181 GATTTCCCTTATGATGCTGCGCCTTTTGGAGACATATTTACCTGAGATGAGAC 240
 QY 394 TGGGCTTTTGGGACATTCCTGCGGAGTGGGCTTTTACGCTGGCCATGAACAGGGCC 453
 DB 241 TGGGCTTTTGGGACATTCCTGCGGAGTGGGCTTTTACGCTGGCCATGAACAGGGCC 300
 QY 454 GGGAGCATGCTGTTCTTACGCTGGTGGCTGCGGACAGTATTTCAAGTGGTCCACCC 513
 DB 301 GGGAGCATGCTGTTCTTACGCTGGTGGCTGCGGACAGTATTTCAAGTGGTCCACCC 360
 QY 514 CACCAAGGGGTAACATATTCACCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 573
 DB 361 CACCAAGGGGTAACATATTCACCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420
 QY 574 GCGCTGATCTCTGGGAAAGTGTATCTTTTCTGGAGAACATCTCTGCTGGAAG 633
 DB 421 GCGCTGATCTCTGGGAAAGTGTATCTTTTCTGGAGAACATCTCTGCTGGAAG 480
 QY 634 AGGCGGCTCTCTGTAAGCTTCAATGAGTGGGCGCAATGGCTGGGACATCATG 693
 DB 481 AGGCGGCTCTCTGTAAGCTTCAATGAGTGGGCGCAATGGCTGGGACATCATG 540
 QY 694 TTCCAGCTGAGTCTTTTATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 753
 DB 541 TTCCAGCTGAGTCTTTTATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
 QY 754 TGGAGCTTGAAGGCGGAGGAGAGCTGCGCAGACAGCTCGATGAAGAGCGG 813
 DB 601 TGGAGCTTGAAGGCGGAGGAGAGCTGCGCAGACAGCTCGATGAAGAGCGG 660
 QY 814 TTTCATATGCTGCTGCAATTTGTTTCAATCAATGCTTACCTGCCAGCGTGTCTGTA 873

DB 661 TTTCATATGCTGCTGCAATTTGTTTCAATCAATGCTTACCTGCCAGCGTGTCTGTA 720
 QY 874 CTCTATTTCTCTGGAAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 933
 DB 721 CTCTATTTCTCTGGAAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
 QY 934 CACATTAACCTCTGAGCTTCACTTACATGAACAGATGCTGATCCCTGGTGTATTTT 993
 DB 781 CACATTAACCTCTGAGCTTCACTTACATGAACAGATGCTGATCCCTGGTGTATTTT 840
 QY 994 TCAAGCCCTCTCTTCCCAATTTCAACAGCTCAAAATGCTGAGTGAACCAAG 1053
 DB 841 TCAAGCCCTCTCTTCCCAATTTCAACAGCTCAAAATGCTGAGTGAACCAAG 900
 QY 1054 CAGCAGAGACCTCAAAACACAAAGGCGGAGAGATGCCAATTTGAACTCGGTGCG 1113
 DB 901 CAGCAGAGACCTCAAAACACAAAGGCGGAGAGATGCCAATTTGAACTCGGTGCG 960
 QY 1114 AGAGATTGATCATGCTGCTGCAATTAAGTTTCAAAAGCAGCTGATGGCAATGGATCC 1173
 DB 961 AGAGATTGATCATGCTGCTGCAATTAAGTTTCAAAAGCAGCTGATGGCAATGGATCC 1020
 QY 1174 CACATTTGATGAGGCACTGA 1194
 DB 1021 CACATTTGATGAGGCACTGA 1041

RESULT 12
 AAD27497
 ID AAD27497 standard; DNA; 1041 BP.
 XX
 AC AAD27497;
 XX
 DT 18-APR-2002 (first entry)
 XX
 DE Human G-protein coupled receptor (GPCRx14) DNA.
 XX
 KW Human; G-protein coupled receptor; GPCRx14; cerebroprotective; vomiting;
 KW receptor-mediated disorder; therapy; urinary retention; allergy; obesity;
 KW osteoporosis; angina pectoris; restenosis; atherosclerosis; hypotension;
 KW anorexia; tumour; migraine; acute heart failure; ulcer; antiinflammatory;
 KW stroke; hypertension; neuronal disorder; myocardial infarction psychotic;
 KW depression; mental retardation; neurodegenerative disease; antibacterial;
 KW Alzheimer's disease; dementia; ischaemia; Parkinson's disease; antiviral;
 KW Huntington's disease; anxiety; antifungal; immunosuppressive; cytostatic;
 KW vulnery; analgesic; anorectic; anabolic; diuretic; cardiant; nootropic;
 KW antiemetic; vasotropic; diabetes; cancer; tranquilizer; neuroleptic; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1041
 FT /tag= a
 FT /product= "Human GPCRx14 protein"
 XX
 XX WO200198330-A2.
 XX
 PD 27-DEC-2001.
 XX
 XX 20-JUN-2001; 2001WO-BE00104.
 PF 20-JUN-2000; 2000US-212913P.
 PR 11-JUL-2000; 2000US-217494P.
 PR 26-JAN-2001; 2001EP-0870015.
 PR 12-FEB-2001; 2001EP-0870024.
 XX
 PA (EURO-) EUROSCREEN SA.
 XX
 PI Lannoy V, Brezillon S, Delheux M, Parmentier M, Govarts C;
 XX
 DR WPI: 2002-130789/17.
 DR P-PSDB; AA017077.
 XX

PT inflammations, including gene therapy -
 XX
 PS Claim 6, Page 94-95; 101pp; Japanese.
 XX
 CC This invention relates to a human lipocyte-originated G protein-coupled
 CC receptor proteins TGR13, thought to be anti-inflammatory and anorectic in
 CC their action. The proteins and encoded DNAs are for use in developing
 CC drugs to treat obesity and inflammation, including gene therapy.
 CC The present sequence represents the human lipocyte-originated G
 CC protein-coupled receptor protein TGR13 encoding sequence.
 XX
 SQ Sequence 1038 BP; 207 A; 294 C; 277 G; 260 T; 0 other;

Query Match 86.8%; Score 1036.4; DB 24; Length 1038;
 Best Local Similarity 99.9%; Pred. No. 2.6e-281;
 Matches 1037; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 154 ATGTCAACGCGGTCGTCGCGGCGGACACATCTCCAGGTATGTCGCGCG 213
 DB 1 ATGTCAACGCGGTCGTCGCGGCGGACACATCTCCAGGTATGTCGCGCG 60
 QY 214 CTGCTCATGTTGGCTTTGCTGCTGCGGCGGACATGAGCAATGGGCTGCTGTTTC 273
 DB 61 CTGCTCATGTTGGCTTTGCTGCTGCGGCGGACATGAGCAATGGGCTGCTGTTTC 120
 QY 274 TGCCTTCACATGAAGACTGGAAGCCAGACTGTTTACCTTTCAATTGGCGGTGCT 333
 DB 121 TGCCTTCACATGAAGACTGGAAGCCAGACTGTTTACCTTTCAATTGGCGGTGCT 180
 QY 334 GATTTCCCTCCCTTATGATCGCTGCTTTGGGACAGATATATCTTACCTGAGATGAGAC 393
 DB 181 GATTTCCCTCCCTTATGATCGCTGCTTTGGGACAGATATATCTTACCTGAGATGAGAC 240
 QY 394 TGGGCTTTTGGGAGACTTCCCTGCGGAGTGGGCTCTTCACTTGGCCATGAACGAGGCC 453
 DB 241 TGGGCTTTTGGGAGACTTCCCTGCGGAGTGGGCTCTTCACTTGGCCATGAACGAGGCC 300
 QY 454 GGGAGCATGTTCTCTTACGAGTGGTGGCTGCGGACAGTATTTTCAAGTGTCCACCC 513
 DB 301 GGGAGCATGTTCTCTTACGAGTGGTGGCTGCGGACAGTATTTTCAAGTGTCCACCC 360
 QY 514 CACCAACGCGGTGAACATATCTCCACCGGGTGGGCGCTGGCATGTCTGCACTCTGTGG 573
 DB 361 CACCAACGCGGTGAACATATCTCCACCGGGTGGGCGCTGGCATGTCTGCACTCTGTGG 420
 QY 574 GCCCTGATCATCTGCGGAAACAGTATCTTTGCTGGAACCATCTCGGCTGCAAGAG 633
 DB 421 GCCCTGATCATCTGCGGAAACAGTATCTTTGCTGGAACCATCTCGGCTGCAAGAG 480
 QY 634 AGGCGCTGCTCTGTGAGAGCTTTCATCATGAGTGGCCATGCTGGCAGACATCATG 693
 DB 481 AGGCGCTGCTCTGTGAGAGCTTTCATCATGAGTGGCCATGCTGGCAGACATCATG 540
 QY 694 TTCAGCTGGAAGTTCTTATGCCCCCTGGCATCATCTTATTTGCTCTTCAAGTTGTT 753
 DB 541 TTCAGCTGGAAGTTCTTATGCCCCCTGGCATCATCTTATTTGCTCTTCAAGTTGTT 600
 QY 754 TGAAGCTGAGCGGAGGAGCAGCTGGCCAGAGGCTCGGATGAAGAAGCGACCGCG 813
 DB 601 TGAAGCTGAGCGGAGGAGCAGCTGGCCAGAGGCTCGGATGAAGAAGCGACCGCG 660
 QY 814 TTCATCATGTTGGGCAATTTGTTTCATCATGCTTACCTGCGAGGCTGCTGCTAGA 873
 DB 661 TTCATCATGTTGGGCAATTTGTTTCATCATGCTTACCTGCGAGGCTGCTGCTAGA 720
 QY 874 CTCCTATTTCTCTGAGAGGTCCTCTGAGTGGCTGCGATCCTCTGTGCAATGGGCGCTG 933
 DB 721 CTCCTATTTCTCTGAGAGGTCCTCTGAGTGGCTGCGATCCTCTGTGCAATGGGCGCTG 780
 QY 934 CACATTAACCTCAGCTTCACTTACATGAACAGCATGCTGATCCCTGATGATATTTT 993
 DB 781 CACATTAACCTCAGCTTCACTTACATGAACAGCATGCTGATCCCTGATGATATTTT 840

QY 994 TCAAGCCCTCTCTTCCCAATTTCTACACAGCTCAAAATCTGCGAGTGAACCCANG 1053
 DB 841 TCAAGCCCTCTCTTCCCAATTTCTACACAGCTCAAAATCTGCGAGTGAACCCANG 900
 QY 1054 CAGCAGAGACACTCAAAACACAAAGCGGAAAGAGATGCAATTTGCAACCTGGTGGC 1113
 DB 901 CAGCAGAGACACTCAAAACACAAAGCGGAAAGAGATGCAATTTGCAACCTGGTGGC 960
 QY 1114 AGGAGTTGATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGATGCC 1173
 DB 961 AGGAGTTGATCAGTGTGGCAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGATGCC 1020
 QY 1174 CACATTGTTAGTGGCAC 1191
 DB 1021 CACATTGTTAGTGGCAC 1038

RESULT 14

AAH50974
 ID AAH50974 standard; DNA; 888 BP.

XX
 AC AAH50974;

XX
 DT 28-AUG-2001 (first entry)

XX
 DE Human nGPCR11 coding sequence #1.

XX
 KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;
 KW signal transduction; schizophrenia; thyroid disorder; renal failure;
 KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
 KW cardiovascular disease; proliferative disorder; hormonal disorder;
 KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 KW attention deficit-hyperactivity disorder/attention deficit disorder;
 KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
 KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 KW neuroprotective; ds.

XX
 OS Homo sapiens.

XX
 PN WO200136473-A2.

XX
 PD 25-MAY-2001.

XX
 PF 16-NOV-2000; 2000MO-US31581.

XX
 PR 16-NOV-1999; 99US-0165838.
 PR 17-NOV-1999; 99US-0166071.
 PR 19-NOV-1999; 99US-016678.
 PR 28-DEC-1999; 99US-0173396.
 PR 22-FEB-2000; 2000US-0184129.
 PR 28-FEB-2000; 2000US-0185421.
 PR 28-FEB-2000; 2000US-0185554.

XX
 PR 02-MAR-2000; 2000US-0186530.
 PR 03-MAR-2000; 2000US-0186811.
 PR 09-MAR-2000; 2000US-0188114.
 PR 17-MAR-2000; 2000US-0190310.
 PR 21-MAR-2000; 2000US-0190800.
 PR 20-APR-2000; 2000US-0198568.
 PR 02-MAY-2000; 2000US-0201190.
 PR 08-MAY-2000; 2000US-0203111.
 PR 25-MAY-2000; 2000US-0207094.

XX
 PA (PHAA) PHARMACIA & UPJOHN CO.

XX
 PI Vogeli G, Wood LS, Parodi LA, Hiesch RR, Lind P, Slightom J;
 PI Scheilin KA, Kayes PS, Bannigan CW, Ruff V, Sejlitz T, Huff RW;
 DR WPI; 2001-389826/41.
 DR P-PDB; AAG80934.

XX
 PT New G protein-coupled receptor (nGPCR-x) and its encoding
 PT polynucleotide useful for diagnosing and treating e.g. schizophrenia -

PS Claim 4; Page 77; 261pp; English.

XX The present invention relates to novel G protein-coupled receptors

CC (NGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,

CC 28, 31-38, 40, 41, 53-60) and their coding sequences. The present

CC sequence is the coding sequence for one such G protein-coupled receptor.

CC GPCRs are also known as seven transmembrane receptors and function in

CC signal transduction. The NGPCRx coding sequences are useful for

CC screening a human to diagnose a disorder affecting the brain or a genetic

CC predisposition, specifically schizophrenia. NGPCRx are useful for

CC identifying compounds useful for treating schizophrenia. Detection of

CC NGPCRx in a sample is useful as a diagnostic tool for diseases or

CC disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,

CC CNS disorders, infections such as HIV-1, metabolic and cardiovascular

CC diseases, proliferative disorders and hormonal disorders. Modulators of

CC NGPCRx activity have the utility for treating neurological disorders,

CC including schizophrenia, ADHD/ADD (attention deficit-hyperactivity

CC disorder/attention deficit disorder), and neuronal disorders such as

CC Alzheimer's disease, Parkinson's disease, migraine and senile dementia.

CC Additional disorders include inflammatory conditions (e.g. Crohn's

CC disease), rheumatoid arthritis, autoimmune disorders, cancers,

CC respiratory ailments such as asthma, and inflammatory diseases e.g.

CC inflammatory bowel disease.

XX

SQ Sequence 888 BP; 174 A; 254 C; 231 G; 229 T; 0 other;

Query Match 74.2%; Score 886.4; DB 22; Length 888;

Best Local Similarity 99.9%; Pred. No. 4e-239;

Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 214 CTGCTCATTTGTCGCTTTGTCGTCGCGCACTAGACGAGGAGTCCGCTGTGTGTTTC 273

DB 1 CTGCTCATTTGTCGCTTTGTCGTCGCGCACTAGACGAGGAGTCCGCTGTGTGTTTC 60

QY 274 TGGCTTCCACATGAGAGCTGGAAGCCGAGCAGCTTTTACCTTTTCAATTTGGCCGTCGTC 333

DB 61 TGGCTTCCACATGAGAGCTGGAAGCCGAGCAGCTTTTACCTTTTCAATTTGGCCGTCGTC 120

QY 334 GATTTCCTCTTATGATCTGCTGCTTTTCGAGACACTATTACCTAGACGCTAGACAC 393

DB 121 GATTTCCTCTTATGATCTGCTGCTTTTCGAGACACTATTACCTAGACGCTAGACAC 180

QY 394 TGGGCTTTTGGGACATTTCCCTGCGAGTGGGCTCTTACGTTGGCCATGAACAGGGCC 453

DB 181 TGGGCTTTTGGGACATTTCCCTGCGAGTGGGCTCTTACGTTGGCCATGAACAGGGCC 240

QY 454 GGGAGCATCGGTTCCCTTACGTTGGTGGCTGGAGACAGGATTTCAAAGTGGCCACCCC 513

DB 241 GGGAGCATCGGTTCCCTTACGTTGGTGGCTGGAGACAGGATTTCAAAGTGGCCACCCC 300

QY 514 CACCACCGGCTGAACACTATCTCCACCAGGAGTGGCTGGACATCGTTCGACCTGTGG 573

DB 301 CACCACCGGCTGAACACTATCTCCACCAGGAGTGGCTGGACATCGTTCGACCTGTGG 360

QY 574 GCCCTGGTCAATCTGGGAAAGTGTATCTTTTGTGGAGAACATCTCTGCTGCAAGAG 633

DB 361 GCCCTGGTCAATCTGGGAAAGTGTATCTTTTGTGGAGAACATCTCTGCTGCAAGAG 420

QY 634 ACGGCGCTCTCTGTGAGAGCTTCATGAGAGTCCGCGCAATGGCTGGACGACATCAG 693

DB 421 ACGGCGCTCTCTGTGAGAGCTTCATGAGAGTCCGCGCAATGGCTGGACGACATCAG 480

QY 694 TTCAGCTGAGAGTTCTTATATGCTCCCTGGGATCATCTTATTTTGTCTCTTCAAGATTGTT 753

DB 481 TTCAGCTGAGAGTTCTTATATGCTCCCTGGGATCATCTTATTTTGTCTCTTCAAGATTGTT 540

QY 754 TGAAGCTTGAAGGGGAGGAGGACAGCTGGCCAGACAGGCTCGATGAAGAAAGGAGCCGG 813

DB 541 TGAAGCTTGAAGGGGAGGAGGACAGCTGGCCAGACAGGCTCGATGAAGAAAGGAGCCGG 600

QY 814 TTGATCATGTGTGTGGGAATTTGTTTCATCATCATGCTACTGCGCCAGCGTGTGCTAAG 873

DB 601 TTGATCATGTGTGTGGGAATTTGTTTCATCATCATGCTACTGCGCCAGCGTGTGCTAAG 660

QY 874 CTCTATTTTCTCTGAGAGTGTCCTCGAGTGCCCTGAGTCCCTCTGTCCATGGAGCCCTG 933

DB 661 CTCTATTTTCTCTGAGAGTGTCCTCGAGTGCCCTGAGTCCCTCTGTCCATGGAGCCCTG 720

QY 934 CACATTAACCTGAGCTTCTACCTACATGAACAGATGCTGGATCCCTGTGTATTTATTTT 993

DB 721 CACATTAACCTGAGCTTCTACCTACATGAACAGATGCTGGATCCCTGTGTATTTATTTT 780

QY 994 TCAAGCCCTCTCTTCCCAATTCTACACAGCTCAAAATCTGACAGTGAACCCAG 1053

DB 781 TCAAGCCCTCTCTTCCCAATTCTACACAGCTCAAAATCTGACAGTGAACCCAG 840

QY 1054 CAGCAGGACACCTCAAAACCAAAAGCCGGAAGAGATGCCAATTTG 1101

DB 841 CAGCAGGACACCTCAAAACCAAAAGCCGGAAGAGATGCCAATTTG 888

RESULT 15

ABK47759

ID ABK47759 standard; CDNA; 1174 BP.

XX

AC ABK47759;

DT 02-JUL-2002 (first entry)

XX

DE cDNA encoding human inflammation-associated GPCR EX20 polypeptide.

XX

KW Human; inflammation-associated G-protein coupled receptor; GPCR; EX20;

KW inflammatory disease; asthma; adult respiratory distress syndrome; ARDS;

KW chronic obstructive pulmonary disease; COPD; bronchitis; emphysema;

KW pneumoconiosis; neutrophil; eosinophil related disorder; airway;

KW lung-related disorder; rheumatoid arthritis; inflammatory bowel disease;

KW ulcerative colitis; skin disease; eczematous dermatitis; gene; ss.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1164

FT /tag= a

FT /product= "inflammation-associated GPCR EX20 polypeptide"

XX

XX W0200213845-A2.

XX

XX 21-FEB-2002.

XX

XX 16-AUG-2001; 2001MO-EP09466.

XX

XX 18-AUG-2000; 2000US-0641653.

XX

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX

XX Jarai G, Yousefi S;

XX

XX WPI; 2002-329542/36.

XX

XX P-PSDB; AAU77992.

XX

XX New pharmaceutical composition comprising EX20 polypeptide, EX20

XX polynucleotide, antibodies against EX20 polypeptide, antisense

XX oligonucleotides against EX20 polynucleotide, useful for treating

XX inflammatory disease -

XX

PS Claim 4; Page 31; 36pp; English.

XX

XX The present invention relates to human inflammation-associated

XX G-protein coupled receptor (GPCR) EX20 polypeptide and the

XX polynucleotide sequence encoding it. A pharmaceutical composition

XX comprising EX20 polypeptide, a variant of EX20, an antibody which

XX immunoreacts with EX20, a polynucleotide encoding EX20 or an antisense

XX oligonucleotide comprising a nucleotide sequence complementary to

XX EX20 can be used in diagnostic and therapeutic applications for

XX treating an inflammatory disease. Such inflammatory diseases include

CC asthma, adult respiratory distress syndrome (ARDS), chronic obstructive
CC pulmonary disease (COPD) including chronic bronchitis, emphysema,
CC pneumoconiosis, neutrophil or eosinophil related disorders, airway and
CC lung-related disorders, rheumatoid arthritis, inflammatory bowel
CC disease, ulcerative colitis, and skin diseases such as eczematous
CC dermatitis. The present sequence encodes human inflammation-associated
CC GPCR EX20 polypeptide.

XX Sequence 1174 BP; 251 A; 336 C; 291 G; 296 T; 0 other;

Query Match 31.3%; Score 374; DB 24; Length 1174;
Best Local Similarity 64.3%; Pred. No. 7.4e-95;

Matches 601; Conservative 0; Mismatches 315; Indels 18; Gaps 2;

Qy 154 ATGTACACGGGTGCTGCTGCGCATGAGGGGACACCATCTCCAGGTGATGCCCGC 213
Db 37 ATAGACAGAAAGACTGCTGTGTTCGAGATGACTTATTGCCAAGGTGTGCCCGC 96
Qy 214 CTGCTATTGTGCTTGTGTGTGGCGCATGAGCAATGGGGTCCCTGTGTGTTTC 273
Db 97 GTGTGGGGCTGAGTTTATCTTTGGGCTTGTGGCAATGGCTTGCCTGTGATTTTC 156
Qy 274 TGCTTCACATGAAGACCTGAGAGCCAGACATGTTTCAATTGGCGGTGCT 333
Db 157 TGTTCACCTCAAGTCTGGAATCAAGCCGATTTCTGTTCACCTGGCAGTACT 216
Qy 334 GATTTCCTCTTATGATCTGCTGCTTTTGGACAGACTATTACTCAAGCTAGACAC 393
Db 217 GACTTCTACTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 276
Qy 394 TGGGCTTTGGGACATTCCTGCGAGTGGGGCTTTCACTTGGCCATGAACAGGGCC 453
Db 277 TGGAGTTTGGGACATTCCTGCGAGTGGGGCTTTCACTTGGCCATGAACAGGGCC 336
Qy 454 GGGAGCATGCTGCTTCTTACGAGTGGGGTGGGACAGGATTTCAAGTGTCCACCCC 513
Db 337 GGGAGCATGATTTCTTCAAGTGGGGTGGGACAGGATTTTCCGGGTGTCCATCCC 396
Qy 514 CACACGCGGTGAACATCTTCCACCGGGTGGGCTGGCATGCTCTGCAACCTGTGG 573
Db 397 CACCAAGCCCTGAACAGATCTTCAATTTGACAGGACATCATCTTCCCTTCTGTGG 456
Qy 574 GCGCTGTGATCTGGGACAGTGTATCTTTTGTGAGAACCAATCTTGGCTGCAAGG 633
Db 457 GGCATCATCTTGGCTTCAAGTGTATCTTCTGAGAACCAATCTTGGCTGCAAGG 516
Qy 634 ACGGCGCTCTCTGAGAGCTTCAATGAGTGGCCATGGCGGACGACATCATG 693
Db 517 ACTGCAAAATGTGTGATCAGCTTTCAGCATCTTCCGATGACGAGATG 576
Qy 694 TTCCAGCTGAGTTCTTTATGCCCCCTGGCATCATTTTGTCTCTTCAAGATTGT 753
Db 577 TTCTCTCTGAGTTCTTCTGCCCCCTGGCATCATCTTGTCTCAAGCAATTTATC 636
Qy 754 TGGAGCTTGAAGGGGAGGAGAGCTGGCCAGAGGCTGGATGAAGAGGCGACCGG 813
Db 637 TGGAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 693
Qy 814 TTTCATCATGTTGGTGGCAATTTGTTTCATCATGTTACCTGCCAGGCTGTCTAGA 873
Db 694 TTTCATCATGTTGGTGGCAATTTGTTTCATCATGTTACCTGCCAGGCTGTCTAGA 753
Qy 874 CTCTATTCTCTGACGGGTGCTC-----GAGTGCCTGCGATCTCT 918
Db 754 ATTCACATCTTCTGGCTCTGACACTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 813
Qy 919 GTTCATGGGGCTTGAACATTAACCTCACTTCACTTCACTTGAAGATGCC 978
Db 814 GTGAGCTGCGCTTCTTTTATCACTTCACTTCACTTCACTTGAAGATGCC 873
Qy 979 CTGGTGTATTTTCAAGCCCTCTTCCCAATTTTCAACAGGCTCAAAATCTGC 1038
Db 874 GTGGGTATCTACTTCCAGCCCATCTTCCCACTTCTTCCACTTGTATCAACCGC 933

Qy 1039 AGCTGAACCCCAAGCAGCCAGGACCTCAAAA 1072
Db 934 TGCTCCAGAGAGATGACAGGTGAGCCAGATA 967

Search completed: April 3, 2003, 21:08:19
Job time : 325 secs

US-07-915-966C-1

Query Match 19.4%; Score 231.2; DB 1; Length 545;
 Best Local Similarity 65.1%; Pred. No. 9.3e-55;
 Matches 357; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

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QY 310 TACCTTTCAATTTGGCCGTGATTTCCCTTATGATCTGCTTCTTTGAGCA 369
DB 1 TTCTGGTGAACCTGCTGGGGCTCACTTTCTCTGATCATTTGGTTCCGTTCTTACG 60
QY 370 GACTATTACCTCAGACGTAGACACTGGGCTTTGGGACATTCCTGCGAGTGGGCTC 429
DB 61 GACCACTATGTCAGAACCTGGAGCTGGAGATTCCTGCGAGATCCCTGCGGATGCTC 120
QY 430 TTCACTTTGGCCATGAAACAGGGCCGGAGCATCTGTTCTTACGCTGCTGCGGAC 489
DB 121 TTCACTTTGGCCATGAAACAGGGCCGGAGCATCTTCTGCACTGCTGCTGCTGAC 180
QY 490 AGGTATTTCAAGTGTCCACCCCGACAGCGGCTGAACACTATCTCCACCGGCTGCG 549
DB 181 AGTACTTCAAGGTGTGTCCACCCCGACAGCATCTTCTGCAACAGATCTCCACCGGCTG 240
QY 550 GCTGGCATCTGTGACACCTGTGGGCTGTGATCTCTGGAAACAGTATCTTTTGTG 609
DB 241 GCACTATCTCTTGTCTTCTGTTGGGCGCATCACTATGCGCTGACATCCCTCTTAC 300
QY 610 GAGAACATCTCTGCTGTGAAGACGCGCTCTCTGTGAGAGCTTCATCATGAGTGC 669
DB 301 ACGGACATGATGACCCGAAACGCGCATGCAAACTGTGAGAGATTTTGAATCTGTAC 360
QY 670 GCCAATGCTGACAGACATCATGTTCCAGTGTGAGTTCTTTATGCCCCCTGGCATATC 729
DB 361 ACTTTAGGTGACAGATGATGATGTTCTCTTGAATTTCTCTGCCCCCTGGCATATC 420
QY 730 TTATTTGCTCTCTTCAAGTTGTTTGAAGCTTGAAGCGGAGGACAGCTGCGCAAG 789
DB 421 CTGTTCTGCTGTGGCAGATTCATTTGAGACCTTAAGGCAAG--ACAGTGAACGAGAC 477
QY 790 GCTCGGATGAAGAGGCGACCCGGTTCATCATGCTGAGTGGCAATGTTGTTCACTAC 849
DB 478 GTCAAGATCAAGAGGCGCATCACTTCATCATGAGTGGTTCATTTGCCATCTGC 537
QY 850 TACCTGCC 857
DB 538 TGGCTGCC 545

```

RESULT 2
 US-08-771-182-1
 Sequence 1, Application US/08771182
 Patent No. 5929209

GENERAL INFORMATION:

APPLICANT: Hadcock Dr., John R.
 APPLICANT: Ozenberger Dr., Bradley A.
 APPLICANT: Pausch Dr., Mark H.
 TITLE OF INVENTION: Receptor Identification Method
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:

ADDRESSEE: American Home Products Corporation
 STREET: One Campus Drive
 CITY: Parsippany
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/771,182
 FILING DATE: 20-DEC-1996
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Matthews, Gale F.
 REGISTRATION NUMBER: 32,269
 REFERENCE/DOCKET NUMBER: 31,829-D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-683-2134
 TELEFAX: 201-683-4117

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 545 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Rat
 PUBLICATION INFORMATION:
 AUTHORS: Hadcock Dr., John R.
 AUTHORS: Ozenberger, Bradley A.
 AUTHORS: Dr. Pausch, Mark H.
 TITLE: Receptor Identification Method
 DATE: 20-DEC-1996

US-08-771-182-1

Query Match 19.4%; Score 231.2; DB 2; Length 545;
 Best Local Similarity 65.1%; Pred. No. 9.3e-55;
 Matches 357; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

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QY 310 TACCTTTCAATTTGGCCGTGATTTCCCTTATGATCTGCTTCTTTGAGCA 369
DB 1 TTCTGGTGAACCTGCTGGGGCTCACTTTCTCTGATCATTTGGTTCCGTTCTTACG 60
QY 370 GACTATTACCTCAGACGTAGACACTGGGCTTTGGGACATTCCTGCGAGTGGGCTC 429
DB 61 GACCACTATGTCAGAACCTGGAGCTGGAGATTCCTGCGAGATCCCTGCGGATGCTC 120
QY 430 TTCACTTTGGCCATGAAACAGGGCCGGAGCATCTGTTCTTACGCTGCTGCGAC 489
DB 121 TTCACTTTGGCCATGAAACAGGGCCGGAGCATCTTCTGCACTGCTGCTGCTGAC 180
QY 490 AGGTATTTCAAGTGTGTCCACCCCGACAGCGGCTGAACACTATCTCCACCGGCTGCG 549
DB 181 AGTACTTCAAGGTGTGTCCACCCCGACAGCATCTTCTGCAACAGATCTCCACCGGCTG 240
QY 550 GCTGGCATCTGTGACACCTGTGGGCTGTGATCTCTGGAAACAGTATCTTTTGTG 609
DB 241 GCACTATCTCTTGTCTTCTGTTGGGCGCATCACTATGCGCTGACATCCCTCTTAC 300
QY 610 GAGAACATCTCTGCTGTGAAGACGCGCTCTCTGTGAGAGCTTCATCATGAGTGC 669
DB 301 ACGGACATGATGACCCGAAACGCGCATGCAAACTGTGAGAGCTTTTGAATCTGTAC 360
QY 670 GCCAATGCTGACAGACATCATGTTCCAGTGTGAGTTCTTTATGCCCCCTGGCATATC 729
DB 361 ACTTTAGGTGACAGATGATGATGTTCTCTTGAATTTCTCTGCCCCCTGGCATATC 420
QY 730 TTATTTGCTCTCTTCAAGTTGTTTGAAGCTTGAAGCGGAGGACAGCATGCTGCCAGAC 789
DB 421 CTGTTCTGCTGTGGCAGATTCATTTGAGACCTTAAGGCAAG--ACAGTGAACGAGAC 477
QY 790 GCTCGGATGAAGAGGCGACCCGGTTCATCATGCTGAGTGGCAATGTTGTTCACTAC 849
DB 478 GTCAAGATCAAGAGGCGCATCACTTCATCATGAGTGGTTCATTTGCCATCTGC 537
QY 850 TACCTGCC 857
DB 538 TGGCTGCC 545

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RESULT 3
 US-08-853-194-1

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; Sequence 1, Application US/08853194
; Patent No. 6077666
; GENERAL INFORMATION:
; APPLICANT: Haddock Dr., John R.
; APPLICANT: Ozenberger Dr., Bradley A.
; APPLICANT: Pausch Dr., Mark H.
; TITLE OF INVENTION: Receptor Identification Method
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: NJ
; COUNTRY: United States of America
; ZIP: 06904-0060
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/853,194
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/915,966
; FILING DATE: 17-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsevdos Dr., Estelle J.
; REGISTRATION NUMBER: 31,145
; REFERENCE/DOCKET NUMBER: 31829-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-321-2361
; TELEFAX: 203-321-2971
; TELEX: 710-474-4059
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 545 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rat
; PUBLICATION INFORMATION:
; AUTHORS: Haddock Dr., John R.
; AUTHORS: Ozenberger, Bradley A.
; AUTHORS: Dr. Pausch, Mark
; TITLE: Receptor Identification Method
; DATE: 17-JUL-1992
; US-08-853-194-1

Query Match      19.4% Score 231.2; DB 3; Length 545;
Best Local Similarity 65.1%; Pred No. 9.3e-55;
Matches 357; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

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; Sequence 1, Application US/08955713
; Patent No. 5955308
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: MOONEY, JEFFREY
; APPLICANT: BERGSMAN, DEBK
; APPLICANT: HALSEY, WENDY
; TITLE OF INVENTION: CDNA CLONE HE04D54 THAT ENCODES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,713
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,124
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1594 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-955-713-1

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Db 495 AGGCACTACCTGCTGGARITVTTCTCGACACGAGGCTCATCTCTTT---GCTATNG 551

Qy 746 AGATTGTTGAGCCTGAGGGGGAGACAGACTGCGCCAGACAGGCTCGATTAAAGAG 805

Db 552 TGAGCATTTGGGCTCACCAACCGGAACCGTGTCTGGGGGGGACAGAGCCCGAGAGGG 611

Qy 806 CGACCCGGTTCAATCAGTGTGTGCGCATTTGTTTCATCACATGCTACCTGCCACGCTGT 865

Db 612 CCATCGAGTNCCTGGCCATGGTGAGTGAGTGTCTACACCATCTGGCTTTCTTGCCAGATCA 671

Qy 866 CTGCTAGACTATTTCCTCTGTGAGAGGAGTGCCTCGAGTGCCTGCGAATCCTCTTCCATG 925

Db 672 TCTTTGGATGGCTTCCATGAGTGGTTCCTGTGCTGCTCGCGATTCCTGGACCTCT 721

Qy 926 GGGCCCTGCACATTA-----CCCTCAGCTTCACCTAATGACAGATGCTGATCCCC 979

Db 732 GCACACACCTCTTCATGAGTCCCTCGGCTTCACCTCACTCAACAGTGTCTGTGACCCG 791

Qy 980 TGTGTATTATTTTCAAGCCCTCTTTCCCA 1013

Db 792 TGCTTACTGCTTCTTAGCCCCCAATCTCTCA 825

RESULT 6

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1Sequence 1, Application us/09130749
2Patent No. 6031090
3
4GENERAL INFORMATION:
5
6APPLICANT: SHABON, USMAN
7
8TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
9RECEPTOR (GPR31A)
10
11NUMBER OF SEQUENCES: 2
12
13CORRESPONDENCE ADDRESS:
14ADDRESSEE: RAYNER & PRESTIA
15STREET: P.O. Box 980
16CITY: Valley Forge
17STATE: PA
18
19COUNTRY: USA
20
21ZIP: 19482
22
23COMPUTER READABLE FORM:
24MEDIUM TYPE: Diskette
25COMPUTER: IBM Compatible
26OPERATING SYSTEM: DOS
27
28SOFTWARE: FastSeq for Windows Version 2.0
29
30CURRENT APPLICATION DATA:
31
32APPLICATION NUMBER: US/09130,749
33
34FILING DATE: 07-Aug-1998
35
36CLASSIFICATION: UNKNOWN
37
38PRIOR APPLICATION DATA:
39
40APPLICATION NUMBER: <Unknown>
41
42FILING DATE: <Unknown>
43
44ATTORNEY/AGENT INFORMATION:
45
46NAME: PRESTIA, PAUL F
47
48REGISTRATION NUMBER: 23,031
49
50REFERENCE/DOCKET NUMBER: GP-70513
51
52TELECOMMUNICATION INFORMATION:
53
54TELEPHONE: 610-407-0700
55
56TELEFAX: 610-407-0701
57
58TELEX: 846189
59
60INFORMATION FOR SEQ ID NO: 1:
61
62SEQUENCE CHARACTERISTICS:
63
64LENGTH: 960 base pairs
65
66TYPE: nucleic acid
67
68STRANDEDNESS: single
69
70TOPOLOGY: linear
71
72MOLECULE TYPE: cDNA
73
74SEQUENCE DESCRIPTION: SEQ ID NO: 1:
75
76US-09-130-749-1

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Query Match	11.7%;	Score 139.2;	DB 3;	Length 960;
Best Local Similarity	51.4%;	Pred. No. 3.8e-29;		
Matches 427;	Conservative	0;	Mismatches 388;	Indels 15; Gaps 4;

OY	215	TGCTATTGTGGCCCTTTGTGCTGGAGCCGATCAGGCAATGGGGTGGCCCTGTGTGGTTTCT	27
Db	59	TGCTGGGGCTGGAGTGTGGCTGGGTTCTGTCTGGGCAAGCGGTGGCGCTGTGAGACTTCC	118
OY	215	GCTTCACATGAAGAAGCTGGAAGCCAGACATGTTTACCTTTTCAATTGGGCGGTGGCTG	33
Db	119	TGTTTCGGGGTACGAGGTGTGGAAAGCCGATACGCTGTCTTACCTCTCAACCTGGACCTGGGTG	178
OY	335	ATTTCCTCTTATATATCTGGCCGCTTTTGGGACAGACTATTTACTCAGAGGTGACACT	39
Db	179	ACCTGCTTTTGGCTGGCGGCTGGCTCTTTCTGGCCGCTTCTTACTAGAGCTCCAGGCTT	238
OY	335	GGGCTTTTGGGAGACATTCCTCGCCGAGAGTGGGGGCTCTTACAGTTGGCCATGAACAGGGCG	45
Db	239	GGCACTGGGCGGTGTGGGGCTGTCTGGGCGCTGGCCCTTCTGTGAGACTCAGCCGACGC	29
OY	455	GGAGCATGTGTCTTCTTAAGGTGTGTGTGCGGACAGTATTTCAAGTGTGCACCCCC	514
Db	299	TGGGATAGGCTCTCTTGGCCCGCTGGCTTTTGAACCGGTACTCTCGTGTGTCCACCCTC	358
OY	515	ACCAAGCGGGTAAACATATCTCCACCCGGGGGGGGCGGTGATGTGTGACCTGTGGG	574
Db	359	GGCTTAAGGTAAACCTGTGTCTTCTTAAGGGGGCTTGGGGGTGTGGGGCTGTGTGGC	418
OY	575	CCCTGTGATCTGAGGAACAGTGTATCTTTTGTGCTGAGAAACATCTGTGGTGCAGAGA	634
Db	419	TCTGTATGTGTGGCCCTACCGCCCGGGCTTGTGTCTGTGAGGGCGGCCAGAACTTCCA	478
OY	635	CGGCGCTCTCTGTGAGAGCTTATCATATGAGTGGC-----CAATGGCTGGCAGACA	688
Db	479	CCAGGTGCACAGTTTCTATCTCCAGGGACAGCGGCTCTTACAGATCATCTGGCAGAGAG	538
OY	689	TCAATGTTCCAGCTGAGGTCTTATATGGCCCTCGGACATCTTATTTGTGCTTCAAGA	748
Db	539	CACCTCTCTGCTTCAAGTTTGTCTCTCCCTTTTGGCTTCACTGTGTGTTCGAATGACAGCA	588
OY	749	TTGTTTGAAGCTGAGGCGGAGG---CAGAGCTGGCCAGACAGGCTCGGATGAAGAG	805
Db	599	TCAATCAGGGCTCTCCAGAAAAAGATCTCGGGAGGCTTGAGAAACAGCCCAACTTCAGGGG	658
OY	806	CGACCCGGTTCATATAGTGTGTGGCAATTGTGTTCATCATCATATGCTTACCTCCACGCTGT	865
Db	659	CCCAAGGACATGTGTACCTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	718
OY	866	CTGTCTAAGCT-CTATTTCTCTGTGAAGGTGCTCCGAGTCCGTCAGATCTCCTGTGTCAT	924
Db	719	TGGGCAAGTGTCTGATGACATCTTCCAGAACTTGGGAGCTGACAGGCGCTTTTGTGCAG	778
OY	925	GGGGCCCT---GCACATACCTCTAGTTTCACTTACATGAACAGCATGTGGATCC	979
Db	779	TGGCTCAATCTCGAATGTACAGGGGAGCTCTACATCACTGCAACAGTGTCTCAACCCG	838
OY	980	TGGTGTATATTTTCAAGCCCTCTTCCCAATTTTCAACCAAGCTC	1029
Db	839	TGGTATCTGCTTCTCCAGCCCACTTACAGAGCTCTATTCGAGGGCTC	888

RESULT 7

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US-09-130-749-1
/ Sequence 1, Application US/09130749
/ Patent No. 6031344
/
/ GENERAL INFORMATION:
/
/ APPLICANT: SHABON, USMAN
/
/ APPLICANT: ELSHOUBAGY, NABIL
/
/ TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
/
/ TITLE OF INVENTION: RECEPTOR (GPR31A)
/
/ NUMBER OF SEQUENCES: 2
/
/ CORRESPONDENCE ADDRESS:
/
/ ADDRESSEE: RATNER & PRESTIA
/
/ STREET: P.O. Box 980
/
/ CITY: Valley Forge
/
/ STATE: PA

```

COUNTRY: USA
 ZIP: 19482
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/130,749
 FILING DATE: 07-AUG-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F.
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GP-70513
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 960 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-130-749-1

Query Match 11.7%; Score 139.2; DB 3; Length 960;
 Best Local Similarity 51.4%; Pred. No. 3.8e-29;
 Matches 427; Conservative 0; Mismatches 388; Indels 15; Gaps 4;

215 TGTCTATTGTGCTTTGCTGCGGCGCACTAGGCAATGCGGCTCGCTGTGTTCT 274
 59 TGCTGGGCGTGGAGTGGGCTGGTCTGCTGGCAACGCGGCTGTGGACCTTCC 118
 275 GCTTCCAGTGAAGACCTGGAACCCAGACACTGTTTACCTTTTCAATTTGGCGTGG 334
 119 TGTTCGGGTCAGGCTGTGGAACCCGTAAGCTTCTTACCTGCTCAACCTGGCCCTGG 178
 335 ATTTCCTTATGATCTGCTGCTCTTTTGGACAGACTTATCACTCAAGCGTACACT 394
 179 ACCTGCTGTGGCTGCTGCTGCTCTTCTTGGCCGCTTCTTACCTGAGACCTTCCAGGCT 238
 395 GGGCTTTTGGGACATTCCTGCGGAGTGGGCTTTTCACTGTCGATGAACAGGCGCG 454
 239 GGCATCTGGGCGCTGTGGGCTGTGGGCTGCGCTTCTGCTGACCTCAGCGCGAGCG 298
 455 GGAAGATCGTGTCTTACGCTGTGGCTGGCGGACAGGTAATTTCAAGGTCACACCCG 514
 299 TGGGGAATGCGCTTCTGCGCGCGCTGCTTTGACCGGTACCTCGTGTGTCACCTTC 358
 515 ACCACGGGTGAACACTATCTCAACCGGCTGGCGGCTGCGATCTGTCAACCTGTGGG 574
 359 GGTTAAGATCAACCTGCTCTTCTTCAAGCGGCGCTGCGGCGCTGTGCTGTGGC 418
 575 CCTGTGCTATCTGGGAACAGTGTATCTTTTGTGGAAGAACATCTCTGTGTCAGAGA 634
 419 TCTGATGATGCTGCTCCTACCTGCGCGGCTTGTCTATCTGTAGGCGCGCCAGAACTCCA 478
 635 CGGCGCTCTCTGAGAGCTTATCATATGAGTCCG-----CAATGGCTGGCAGACA 688
 479 CCAAGTCCCAAGTTTCTTCTCAAGGCGACAGGCTCTTCAAGATCATCTGCGAGGAAG 538
 689 TCATGTTCCAGTGAAGTCTTATGCTTGTGCGGCACTCATTTATTTTCTCTCTTCAAGA 748
 539 CACTCTCTGCTCACTGTTTGTCTCTCTCTTGTGCTCAACGCTGTCTGGAATGAGGGA 598
 749 TTGTTTGAAGCTTGAGCGGAGG--CAGACGTGGCCAGACAGGCTCGAGTAAGAGCG 805

Db 599 TCATCAGGCGCTTCCAGAAAAGACTCCGGGAGCTTGAGAAACAGCCCAAGCTTCAAGCGG 658
 Qy 806 CGACCCGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 865
 Db 659 CCAGGCACTGTGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 718
 Qy 866 CTGCTAAGTCTTATTTCTTGAAGGATGATGATGATGATGATGATGATGATGATGAT 924
 Db 719 TGGCAGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 778
 Qy 925 GGGGCTT-----GCACATACCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTT 979
 Db 779 TGGCTCATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 838
 Qy 980 TGGTATATTTTTCAGGCTTCTTCCCAATTTCTTCAAGTCTTCAAGTCTTCAAGTCTT 1029
 Db 839 TGTATATCTTCTTCTTCCAGCCCACTTCAAGGATCTTATGAGAGGATC 888

RESULT 8
 US-08-153-848-43
 Sequence 43; Application US/08153848
 Patent No. 5759804
 GENERAL INFORMATION:
 APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schwellart, Vicki L.
 TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Bicknell
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/153,848
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,452
 FILING DATE: 17-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5759804and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1901 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 701..1717
 US-08-153-848-43

Query Match 9.3%; Score 110.6; DB 1; Length 1901;
 Best Local Similarity 47.2%; Pred. No. 4.4e-21;
 Matches 378; Conservative 0; Mismatches 414; Indels 9; Gaps 1;

201 GGTGATGCGCGCGCTGCTCATTTGTCCTTTGTGTCGGCGCATAGGCAATGGGGTCG 260
 Db GGTGATGCGCGCGCTGCTCATTTGTCCTTTGTGTCGGCGCATAGGCAATGGGGTCG 260
 796 GGTGATGCGCGCGCTGCTCATTTGTCCTTTGTGTCGGCGCATAGGCAATGGGGTCG 260
 261 CCGTGTGCTTTCTGCTTCCATGATGAGCCGGAAGCCAGCATGTTTACCTTTTCAA 320
 Db CCGTGTGCTTTCTGCTTCCATGATGAGCCGGAAGCCAGCATGTTTACCTTTTCAA 320
 856 TCTGTGCTTTCTGCTTCCATGATGAGCCGGAAGCCAGCATGTTTACCTTTTCAA 320
 321 TTTGGCCGTGCTGATTTCTCTTATGATGCTGCTGCTTTTGGACAGATTTACT 380
 Db TTTGGCCGTGCTGATTTCTCTTATGATGCTGCTGCTTTTGGACAGATTTACT 380
 916 TCTGCGCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 975
 381 CAGAGTGAACACTGGGCTTTTGGGGAATTCCTGCGGAGTGGGGCTTTCACTTGGC 440
 Db CAGAGTGAACACTGGGCTTTTGGGGAATTCCTGCGGAGTGGGGCTTTCACTTGGC 440
 976 CTCTGGGAACCACTGGGCTTTTGGGGAATTCCTGCGGAGTGGGGCTTTCACTTGGC 440
 441 CATGAACAGGCGCGGAGCATGCTGCTTACGATGCTGCTGCTGCTGCTGCTGCT 500
 Db CATGAACAGGCGCGGAGCATGCTGCTTACGATGCTGCTGCTGCTGCTGCTGCT 500
 1036 CCGTCAACATGATGAGCCGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1095
 501 AGTGTGCAACCCCAACCAAGCGGTGAACATATCTTCAACCGGGTGGCGGCTGATCT 560
 Db AGTGTGCAACCCCAACCAAGCGGTGAACATATCTTCAACCGGGTGGCGGCTGATCT 560
 1096 CATGTGTGCAACCCCAACCAAGCGGTGAACATATCTTCAACCGGGTGGCGGCTGATCT 560
 561 CTGACCCCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
 Db CTGACCCCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
 1156 TGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1215
 621 CTGCGTGAACAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
 Db CTGCGTGAACAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680
 1216 CCGTCAACATGATGAGCCGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1275
 681 GCAGACATATGTTTCAAGCTGAGTTCTTATGCTGCTGCTGCTGCTGCTGCTGCT 740
 Db GCAGACATATGTTTCAAGCTGAGTTCTTATGCTGCTGCTGCTGCTGCTGCTGCT 740
 1276 TGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1335
 741 CTGCAAGATGTTTGAAGCCGATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 800
 Db CTGCAAGATGTTTGAAGCCGATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 800
 1336 CCGTCAACATGATGAGCCGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1395
 801 GAAGGCGACCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 851
 Db GAAGGCGACCGGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 851
 1396 GCGAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1455
 852 CCGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911
 Db CCGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911
 1456 CCGTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1515
 912 TCCCTGCTGATGAGGCGCTGACATGATGATGATGATGATGATGATGATGATGATGAT 971
 Db TCCCTGCTGATGAGGCGCTGACATGATGATGATGATGATGATGATGATGATGATGAT 971
 1516 GCGATGCTGAGGCGCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 1575
 972 GATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 992
 Db GATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 992
 1576 GATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1596

RESULT 9

US-09-299-843A-43
 ; Sequence 43, Application US/09299843A
 ; Patent No. 6107475
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schmelkare, Vicki L.
 ; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSES: Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois

COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/299,843A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/088,337
 FILING DATE: 01-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/153,848
 FILING DATE: 17-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,452
 FILING DATE: 17-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: JILL E. UHL
 REGISTRATION NUMBER: 43,213
 REFERENCE/DOCKET NUMBER: 27866/32059B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX:
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1901 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE TYPE: DNA (genomic)
 NAME/KEY: CDS
 LOCATION: 701..1717
 US-09-299-843A-43

Query Match 9.3%; Score 110.6; DB 3; Length 1901;
 Best Local Similarity 47.2%; Pred. No. 4,4e-21;
 Matches 378; Conservative 0; Mismatches 414; Indels 9; Gaps 1;
 201 GGTGATGCGCGCGCTGCTCATTTGTCCTTTGTGTCGGCGCATAGGCAATGGGGTCG 260
 Db GGTGATGCGCGCGCTGCTCATTTGTCCTTTGTGTCGGCGCATAGGCAATGGGGTCG 260
 796 GGTGATGCGCGCGCTGCTCATTTGTCCTTTGTGTCGGCGCATAGGCAATGGGGTCG 260
 261 CCGTGTGCTTTCTGCTTCCATGATGAGCCGGAAGCCAGCATGTTTACCTTTTCAA 320
 Db CCGTGTGCTTTCTGCTTCCATGATGAGCCGGAAGCCAGCATGTTTACCTTTTCAA 320
 856 TCTGTGCTTTCTGCTTCCATGATGAGCCGGAAGCCAGCATGTTTACCTTTTCAA 320
 321 TTTGGCCGTGCTGATTTCTCTTATGATGCTGCTGCTTTTGGACAGATTTACT 380
 Db TTTGGCCGTGCTGATTTCTCTTATGATGCTGCTGCTTTTGGACAGATTTACT 380
 916 TCTGCGCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 975
 381 CAGAGTGAACACTGGGCTTTTGGGGAATTCCTGCGGAGTGGGGCTTTCACTTGGC 440
 Db CAGAGTGAACACTGGGCTTTTGGGGAATTCCTGCGGAGTGGGGCTTTCACTTGGC 440
 976 CTCTGGGAACCACTGGGCTTTTGGGGAATTCCTGCGGAGTGGGGCTTTCACTTGGC 440
 441 CATGAACAGGCGCGGAGCATGCTGCTTACGATGCTGCTGCTGCTGCTGCTGCT 500
 Db CATGAACAGGCGCGGAGCATGCTGCTTACGATGCTGCTGCTGCTGCTGCTGCT 500
 1036 CCGTCAACATGATGAGCCGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1095
 501 AGTGTGCAACCCCAACCAAGCGGTGAACATATCTTCAACCGGGTGGCGGCTGATCT 560
 Db AGTGTGCAACCCCAACCAAGCGGTGAACATATCTTCAACCGGGTGGCGGCTGATCT 560
 1096 CATGTGTGCAACCCCAACCAAGCGGTGAACATATCTTCAACCGGGTGGCGGCTGATCT 560
 561 CTGACCCCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
 Db CTGACCCCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620
 1156 TGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1215
 621 CTGCGTGAACAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 680


```

APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schenkart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noiland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 701..1717
PCT-US93-11153-43

Query Match          9.3%; Score 110.6; DB 5; Length 1901;
Best Local Similarity 47.2%; Pred. No. 4.4e-21;
Matches 378; Conservative 0; Mismatches 414; Indels 9; Gaps 1;

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QY 561 CTGACACCTGTGGGCGCTGTGATCTCTGGAAACAGTATCTTTTGTGGAAACCATCT 620
DB 1156 TCCCTTCCTGTGGGAGTGTGTGGCTGTGGCCATGGCCCCGTGCTGTGGAGCCACAGAC 1215
QY 621 CTGCGTGAAGAGACGCGCTCTCTGTGAAGCTTCATCATGAGTGGCCAAATGGCTG 680
DB 1216 CGTGAGACCAACACACAGGTGTCTGCTCAGCTGACGGAGAAAGGCTCCACCA 1275
QY 681 GCAGACATCATGTTCCAGCTGAGATCTTTATGCCCCCTGGCATCATCTTATTTGCTC 740
DB 1276 TGCCCTGTGTCCCTGAGAGTGGCTTACCTTCCCTTCATCACACAGGTACCTGCTA 1335
QY 741 CTTCAGATTGTTTGAAGCTGAGCGAGGACAGACGCTGCGACAGCTCGGATGAA 800
DB 1336 CCGTGTGATCATCCGACCTCTGGCAGAGGCTGCTGTGTGAGAAAGCCCTCAAGACCA 1395
QY 801 GAAGCGACCCGGTTCATCATGTGTGTGCAATTGT-----GTTCATCATGCTGA 851
DB 1396 GGCAGTGGCATGATCGCATATGTGCTGGCCATCTTCTGTGTGCTTGTGCTTACCA 1455
QY 852 CCGGCCAGCGCTGTCTGTACATCTTATTTCTGTGACGTGCTTGAAGTCTTGGGA 911
DB 1456 CGTCAACCGCTCCGTCTTACGTGTGCACTACCGAGCCATGGGCTCTTGGCCACCA 1515
QY 912 TCCCTGTCCATGGGCGCTGCAATACCTCAGCTTCACTCACTCAAGAACAGCATGCT 971
DB 1516 GCGCATCTGTGGCCCTGGCAACCCGATACCTCTGCTTCCACAGCTCAAGGGGCACT 1575
QY 972 GGATCCCTGGTGTATATT 992
DB 1576 CGACCCCATCATGATTTCTT 1596

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RESULT 12
PCT-US95-07180-1
Sequence 1, Application PC/RUS9507180
GENERAL INFORMATION:
APPLICANT: LI, XI
APPLICANT: GOCAYNE, JEANINE D
APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBB69
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NJ
COUNTRY: US
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

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FEATURE:
NAME/KEY: CDS
LOCATION: 548..1564
PCT-US95-07180-1

Query Match 9.3%; Score 110.6; DB 5; Length 2453;
Best Local Similarity 47.2%; Pred. No. 5e-21;
Matches 378; Conservative 0; Mismatches 414; Indels 9; Gaps 1;

201 GGTGATGCCGCGCTGCTCATTTGTCCTTTGTCGCGGCGCATAGCAATGGGGTGC 260
643 GCGTGTGCGCTCTTCTACCTTGTGATTTTATCTGCGCTTATGTCGCAATACCTTGC 702
261 CTTGTGTGTTTCTGTTTCCATATGAAGCTCGAAGCCGACACTGTTTACCTTTGCA 320
703 TCTGTGCTTTTCTATCCAGACCAAGTCCGAGACCCGCGCAACGTTCTATGCA 762
321 TTTGGCGGTGCTGATTTCTCTTATGATCTGCTGCTTTTCCGAGAAGTATTA 380
763 TCTGCGCGTGGCGGACTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 822
381 CAGACGTAGACACTGGGCTTTTGGGACATTCCTGCGAGTGGGGCTTTACGTTGGC 440
823 CTCTGGAACCACTGGGCTATTTGGGGAATTCGATGCCCTTCTACCGGCTTCTCTTA 882
441 CATTGACAGGCGCGGAGCATGTTCTTATGCGTGGTGGTGGTGGGACAGGATTTGCA 500
883 CTTCAACATGTAAGCCAGCATCTACTTCTTCACTGATCAGCGCGGACCGTTTCTGGC 942
501 AGTGTCAACCCCAACCAACGCGGTGAACATACTTCCACCCGCGTGGCGGATGATGAT 560
943 CATTGTGACACCGGTGCAATGCTTCTCAAGCTCCGAGGCGCTTCAAGCAACCTGAGCTG 1002
561 CTGACACCTGTGGGCGCTGATCTCTGGGAACATGTTCTTTTCTGTTGGAACCACT 620
1003 TGCCTTCTCTGTGGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1062
621 CTGCGTGAAGAGAGAGCGGCTCTCTGATGAGCTTCACTGATGAGTGGCCATAGGCTG 680
1063 CTTGACACCAACCAACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1122
681 GCAACGATCATGATTCAGCTGAGTCTTATATGCCCCCTGCGATCATTTATTTTGTCT 740
1123 TGCCTGTGTGCTCTGAGAGTGGCTTCACTTCCGTTCAACACAGCTGACCTGCTA 1182
741 CTTCAAGATTTTGTGAGCTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 800
1183 CTTGCTGATCATCCGACGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1242
801 GAGGAGAGCGGCTTCACTATGATGATGATGATGATGATGATGATGATGATGATGAT 851
1243 GCGAGTGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1302
852 CTTGCCAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 911
1303 CTTCAACGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1362
912 TCCCTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 971
1363 GCGCATCTGCGGCTGCGCAACCGCATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1422
972 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 992
1423 GAGACCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1443

RESULT 13
US-08-724-974A-1
Sequence 1, Application US/08724974A
Patent No. 591335
GENERAL INFORMATION:
APPLICANT: Derek J. Bergama, Catherine E. Ellis
TITLE OF INVENTION: A No. 591235el G-Protein Coupled Receptor

TITLE OF INVENTION: HIVCT136
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,974A
FILING DATE: October 3, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEFAX: 610 270 5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1597
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: No
US-08-724-974A-1

Query Match 8.9%; Score 105.8; DB 2; Length 1597;
Best Local Similarity 47.0%; Pred. No. 8.8e-20;
Matches 400; Conservative 0; Mismatches 442; Indels 9; Gaps 2;

158 ACAAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 217
361 ACACTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
218 TCAATGAGGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 274
421 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
275 GCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 334
481 ACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
335 ATTTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 394
541 ACCTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
395 GGGCTTTTGGGAGCATCTCTGCGAGTGGGGCTCTTCAAGTTGGGCGATGAACAGGCGCG 454
601 GGTTCACGGGAGCTTCTCTGCGAGTGGGGCTCTTCAAGTTGGGCGATGAACAGGCGCG 660
455 GAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 514
661 TCAAGTGGGCTTCTCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
515 ACACGCGGTGAACATATCTTCAACCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 574
721 TCCGCTTCAACAGTTCCGAGCTCTGAAGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 780
575 CCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 634
781 CCAAGAGCTGCTGACCAAGATCTACTTCTGATGACAGAGAGGTGATGAGAGAGAGAG 840

QY 635 -----CGCCGCTCTCTGTGAGAGCTTCATCATGAGTGGCCAAATGGCTGGACGACA 688
 Db 841 ACCAGCACCGGCTGTGCTTTAGCACTACCCCATCCAGGATGGAGAGCGCCATCAACT 900
 QY 689 TCATGTTCCAGGTGAGTCTTTATAGCCCCCTCGCATATCTTATTTGCTCTTCAAGA 748
 Db 901 ACTACCGCTTCTCCGTGGGCTTCTCTTCCCATCTGCTGCTGCGCTGCTTACCAAG 960
 QY 749 TTGTTTGGAGCTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 808
 Db 961 GCATCTGCGGCGCGGTGGCGGAGCCAGGACCCAGAGAGCGGAGAGGAGGAGGAGGAG 1020
 QY 809 CCGCGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 868
 Db 1021 AGCGCGTGTCTGAGCAAGCGGTGATCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCT 1080
 QY 869 CTAGACTATTTCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 928
 Db 1081 TGCTGCTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
 QY 929 CCCTGCAATACCTGAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 988
 Db 1141 CCTACCACTTCTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 QY 989 ATTTTCAAGC 999
 Db 1201 GCTTGTGACG 1211

RESULT 14
 US-08-442-134A-1
 ; Sequence 1, Application US/08442134A
 ; Patent No. 5596088
 ; GENERAL INFORMATION:
 ; APPLICANT: Boucher, Richard C.
 ; APPLICANT: Weisman, Gary A.
 ; APPLICANT: Turner, John T.
 ; APPLICANT: Harden, Thomas K.
 ; APPLICANT: Parr, Claude E.
 ; APPLICANT: Sullivan, Daniel M.
 ; APPLICANT: Erb, Laura
 ; APPLICANT: Lustig, Kevin D.
 ; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
 ; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bell, Selzer, Park & Gibson
 ; STREET: Post Office Drawer 34009
 ; CITY: Charlotte
 ; STATE: No. 5596088ch Carolina
 ; COUNTRY: USA
 ; ZIP: 28234
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/442,134A
 ; FILING DATE: 16-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sibley, Kenneth D.
 ; REGISTRATION NUMBER: 31,665
 ; REFERENCE/DOCKET NUMBER: 5470-71A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-420-2200
 ; TELEFAX: 919-881-3175
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1842 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 57..1181
 ; US-08-442-134A-1

Query Match
 Best Local Similarity 7.8%; Score 92.6; DB 1; Length 1842;
 Matches 215; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

QY 163 GGATGCTGTGCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 222
 Db 120 GGCTACAGGTGCGGCTTCAACAGAGGATCAAGTACGCTGCTGCTGCTGCTGCTGCTGCT 179
 QY 223 GTGCGCTTTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 282
 Db 180 GTGAGTGTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 239
 QY 283 ATGAAGACCTGGAAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 342
 Db 240 CTCAAGACCTGGAATGCTGCAACAGATATATGTTCCACTGCTGTGTGATGACACTG 299
 QY 343 CTATGATCTGCTGCTGCTTTCGAGAGACTATTACCTGAGAGGAGGAGGAGGAGGAGGAG 402
 Db 300 TATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 359
 QY 403 GGGAGCATTTCCCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 462
 Db 360 AGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 419
 QY 463 GTGTTCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 522
 Db 420 CTCTTCTTCACTGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 479
 QY 523 GTGAACATATCTCCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 581
 Db 480 CTGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 538

RESULT 15
 US-08-444-581B-1
 ; Sequence 1, Application US/08444581B
 ; Patent No. 5607836
 ; GENERAL INFORMATION:
 ; APPLICANT: Boucher, Richard C.
 ; APPLICANT: Weisman, Gary A.
 ; APPLICANT: Turner, John T.
 ; APPLICANT: Harden, Thomas K.
 ; APPLICANT: Parr, Claude E.
 ; APPLICANT: Sullivan, Daniel M.
 ; APPLICANT: Erb, Laura
 ; APPLICANT: Lustig, Kevin D.
 ; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
 ; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bell, Selzer, Park & Gibson
 ; STREET: Post Office Drawer 34009
 ; CITY: Charlotte
 ; STATE: No. 5607836ch Carolina
 ; COUNTRY: USA
 ; ZIP: 28234
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/444,581B
 ; FILING DATE: 19-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/442,134
FILING DATE: 16-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 57..1181
US-08-444-581B-1

Query Match 7.8%; Score 92.6; DB 1; Length 1842;
Best Local Similarity 51.3%; Pred. No. 4.3e-16;
Matches 215; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

QY 163 GGGTGTGTGCGCGATGAGGGGAGACCATCTCCAGGTATGCCGCGTGTCTATT 222
DB 120 GGGTACAGGTGCGGCTTCAACGAGACTTCAAGTGTGTGCTGTCTTCTACGGC 179
QY 223 GTGGCTTTGTGTGGGGGCACTAGGCAATGGGTGGCCCTGTGTGATTTCTGCTTCAC 282
DB 180 GTGGTGTGTGTCTGTGGGTGTGTGTGAACGGCGGTGACCTTACATCTTGTGGCCG 239
QY 283 ATGAAGCTGGAAGCCAGCACTGTTAAGTTTCAATTGGCCGTGCTGATTTCTC 342
DB 240 CTCAGACCTGGAATGCCGTCACCATATATGTTCCACTGGCTGTGTGATGCACTG 299
QY 343 CTTATGATCTGCTGCTTTTGGACAGCTTTAAGTCAAGCTAGACCTAGACCTGCTTT 402
DB 300 TATGGGCTCTCCCTGCGCTGTGTGTATTTCTAGCGCCGCGACCACTGGCCCTTC 359
QY 403 GGGGACATTCCTGCGGAGTGGGGCTTTACAGTTGGCCATGACAGGGCCGGAGCATC 462
DB 360 AGCAGGTGTCTGTGCAAGCTGGTGGGCTTCTCTTACACCACTTTACTGCAGCATC 419
QY 463 GTGTTCTTACAGGTGTGCTGCGAGAGATTTCAAGTGTTCACACCCACACCGCG 522
DB 420 CTTTCTTCACTGATGACGCGTGCACCGGTGTGGGGCTTTACGACCTTGTGCTTC 479
QY 523 GTGAACATATCTCCACCGGGGTGGCGGCTGATGACCTGTGGGCTTGTGT 581
DB 480 CTGGCTGGGGCGGGCCGCTACGCTGCCCGGGTGGCCGCTGTGGGTGTGTGT 538

Search completed: April 3, 2003, 22:47:29
Job time : 70 secs

11

QY 181 GAGGGGGAACACATCTCCAGGTGATGCGCCGCTGCTCATTTGAGCCCTTTGTGCGGC 240
 DB 181 GAGGGGGAACACATCTCCAGGTGATGCGCCGCTGCTCATTTGAGCCCTTTGTGCGGC 240
 QY 241 GCAGTAAAGGCAATGGGGTGCCTGTGTGATTTCTGCTTCCATGAAAGACCTGGAAAGCC 300
 DB 241 GCAGTAAAGGCAATGGGGTGCCTGTGTGATTTCTGCTTCCATGAAAGACCTGGAAAGCC 300
 QY 301 AGCAGCTGTTTAACTTTTCAATTTGGCCGTGTGATTTCTTCCCTTAAATGATCTGCTGCT 360
 DB 301 AGCAGCTGTTTAACTTTTCAATTTGGCCGTGTGATTTCTTCCCTTAAATGATCTGCTGCT 360
 QY 361 TTTCCGACAGACTATTAATCTGAGAGTGAACACTGGGCTTTTGGGAGATTCCTGCGGA 420
 DB 361 TTTCCGACAGACTATTAATCTGAGAGTGAACACTGGGCTTTTGGGAGATTCCTGCGGA 420
 QY 421 GTGGGGCTTTTCAAGTGTGCAAGAGAGGCGGAGAGATGTTCTTACGCTGTG 480
 DB 421 GTGGGGCTTTTCAAGTGTGCAAGAGAGGCGGAGAGATGTTCTTACGCTGTG 480
 QY 481 GCTGGGGAACAGTATTTCAAGTGTGCAAGAGAGGCGGAGAGATGTTCTTACGCTGTG 540
 DB 481 GCTGGGGAACAGTATTTCAAGTGTGCAAGAGAGGCGGAGAGATGTTCTTACGCTGTG 540
 QY 541 CGGGTGGCGGCTGGCATGCTGTGCAAGAGAGGCGGAGAGATGTTCTTACGCTGTG 600
 DB 541 CGGGTGGCGGCTGGCATGCTGTGCAAGAGAGGCGGAGAGATGTTCTTACGCTGTG 600
 QY 601 CTTTGTGAGAGAACCATCTGTGCTGCAAGAGAGGCGGAGAGATGTTCTTACGCTGTG 660
 DB 601 CTTTGTGAGAGAACCATCTGTGCTGCAAGAGAGGCGGAGAGATGTTCTTACGCTGTG 660
 QY 661 ATGGAGTGGGCAATGGGCTGGGAGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 720
 DB 661 ATGGAGTGGGCAATGGGCTGGGAGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 720
 QY 721 GGCATCATTTATTTTGTCTCTTCAAGATTTTGGAGGCTGGGAGAGAGATGTTCTTACGCTGTG 780
 DB 721 GGCATCATTTATTTTGTCTCTTCAAGATTTTGGAGGCTGGGAGAGAGATGTTCTTACGCTGTG 780
 QY 781 GCCAGACAGGCTGGATGAGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 840
 DB 781 GCCAGACAGGCTGGATGAGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 840
 QY 841 ATCAGATGCTACCTGCGGAGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 900
 DB 841 ATCAGATGCTACCTGCGGAGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 900
 QY 901 AGTGCCTGGATCTCTGTGCTGATGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 960
 DB 901 AGTGCCTGGATCTCTGTGCTGATGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 960
 QY 961 AACAGATGCTGATCTCTGTGCTGATGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 1020
 DB 961 AACAGATGCTGATCTCTGTGCTGATGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 1020
 QY 1021 AACAGATGCTGATCTCTGTGCTGATGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 1080
 DB 1021 AACAGATGCTGATCTCTGTGCTGATGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 1080
 QY 1081 CCGGAGAGAGATGCTGATGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 1140
 DB 1081 CCGGAGAGAGATGCTGATGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 1140
 QY 1141 TTTCAAGGCAATGCTGATGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 1194
 DB 1141 TTTCAAGGCAATGCTGATGAGAGAGGCGGAGAGATGTTCTTACGCTGTG 1194

RESULT 2
 US-10-092-135-1
 ; Sequence 1, Application US/10092135
 ; Publication No. US20030054374A1

; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR.
 ; FILE REFERENCE: D0134.NP
 ; CURRENT APPLICATION NUMBER: US/10/092.135
 ; PRIOR FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US 60/273,808
 ; PRIOR FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/278,983
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: Patent In version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 2580
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (457) .. (1482)
 US-10-092-135-1

Query Match 96.2%; Score 1148.2; DB 9; Length 2580;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 1175; Conservative 1; Mismatches 9; Indels 2; Gaps 2;
 QY 8 CCAACCCACACACACAGAGCCGATCTGGGTGATGAAAGTCAGACACACAGCAGCTGGG 67
 DB 311 CAAACCCACACACACAGAGCCGATCTGGGTGATGAAAGTCAGACACACAGCAGCTGGG 370
 QY 68 TGAAGTCTAAGCTCAGATTAAGATCTGTGCAATGTGAGGAGCTCCCTGGGCTGCTG 127
 DB 371 TGAAGTCTAAGCTCAGATTAAGATCTGTGCAATGTGAGGAGCTCCCTGGGCTGCTG 430
 QY 128 ACCCGGACACCTGTCTGTGCTCCCGGATGATACAGAGGTCGAGTGGCGGATCGAGGGG 187
 DB 431 ACCCGGACACCTGTCTGTGCTCCCGGATGATACAGAGGTCGAGTGGCGGATCGAGGGG 490
 QY 188 ACACCATCTCCAGAGTGAAGCGCGCTGCTCATATTTGAGGCTTTGTGCTGGGCGAGTAG 247
 DB 491 ACACCATCTCCAGAGTGAAGCGCGCTGCTCATATTTGAGGCTTTGTGCTGGGCGAGTAG 550
 QY 248 GCAATGGGATGCGCTGTGTGCTTCTGCTTCAATGAAGACCTGGAAAGCCGAGCATCTG 307
 DB 551 GCAATGGGATGCGCTGTGTGCTTCTGCTTCAATGAAGACCTGGAAAGCCGAGCATCTG 610
 QY 308 TTTACCTTTCAATTTGGCGGTGGCTGATTTCTCTTAAATGATGCGGCTTTTCGGA 367
 DB 611 TTTACCTTTCAATTTGGCGGTGGCTGATTTCTCTTAAATGATGCGGCTTTTCGGA 670
 QY 368 CAGACTTATCTCAGACGTAGACACTGGGCTTTTGGGAGCAATTCCTTCCGAGAGTGGG 427
 DB 671 CAGACTTATCTCAGACGTAGACACTGGGCTTTTGGGAGCAATTCCTTCCGAGAGTGGG 730
 QY 428 TCTTACGTTGGCCATGAAAGAGGCGGAGAGATGCTGTGCTTAAAGGTGTGCTGCGG 487
 DB 731 TCTTACGTTGGCCATGAAAGAGGCGGAGAGATGCTGTGCTTAAAGGTGTGCTGCGG 790
 QY 488 ACAGATTTTCAAGTGTGCAACCCGACAGCGGAGTGAACCTATCTCAACCGGAGTGG 547
 DB 791 ACAGATTTTCAAGTGTGCAACCCGACAGCGGAGTGAACCTATCTCAACCGGAGTGG 850
 QY 548 CGGCTGATCTGTGCAACCTGTGGGCTTGTGCTCACTCTGGGAGACAGTGTATCTTTTGC 607
 DB 851 CGGCTGATCTGTGCAACCTGTGGGCTTGTGCTCACTCTGGGAGACAGTGTATCTTTTGC 910
 QY 608 TGAAGAACATCTCTGTGCTGAAAGAGAGCGGCTTCTCTGTGAGAGCTTCAATATGAGT 667
 DB 911 TGAAGAACATCTCTGTGCTGAAAGAGAGCGGCTTCTCTGTGAGAGCTTCAATATGAGT 970
 QY 668 CGGCAATGCTGGACAGACATCATGTTCCAGTGAAGTCTTTATGAGGCTCGGAGTGA 727
 DB 971 CGGCAATGCTGGACAGACATCATGTTCCAGTGAAGTCTTTATGAGGCTCGGAGTGA 1030


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QY 728 TCTATTGCTCTCTTCAAGATTGTTTGAAGCCTGAGCGGAGGACAGACTGCGGACAG
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Db 1031 TCTATTGCTCTCTTCAAGATTGTTTGAAGCCTGAGCGGAGGACAGACTGCGGACAG
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QY 788 AGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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|
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Db 1091 AGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 848 GCTACCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 1151 GCTACCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 908 GCGATCCTCTGTCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 1211 GCGATCCTCTGTCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 968 TGGTGGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 1271 TGGTGGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 1028 TCAAAATCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 1331 TCAAAATCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 1088 AGATGCGCAATTTGGAACCTGCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 1391 AGATGCGCAATTTGGAACCTGCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 1148 GCCAGTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 1450 GCCAGTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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RESULT 3
US-09-942-374-3
; Sequence 3, Application US/09942374
; Patent No. US20020137063A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Giorno, Ruth
; APPLICANT: White, David
; TITLE OF INVENTION: Receptor Family Member and Uses Therefor
; FILE REFERENCE: MPI2000-368P/R
; CURRENT APPLICATION NUMBER: US/09/942,374
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/228,409
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: human
US-09-942-374-3

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Query Match      87.2%; Score 1041; DB 10; Length 1041;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 154 ATGTACAAAGGAGTGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 1 ATGTACAAAGGAGTGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 214 GTGCTCATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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|
Db 61 CTGCTCATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 274 TGGCTTCCACATGAAGACCTGGAAGCCGACGACTGTTTACCTTTTCAATTGCGCGTGGCT
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Db 121 TGGCTTCCACATGAAGACCTGGAAGCCGACGACTGTTTACCTTTTCAATTGCGCGTGGCT
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QY 334 GATTTCTCTTATGATGCTGCTGCTTTTGGACAGACTATTTCTCAGAGCTAGAC
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Db 101 GATTTCTCTTATGATGCTGCTGCTTTTGGACAGACTATTTCTCAGAGCTAGAC
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QY 394 TGGGCTTTGGGAGACATTCCTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 241 TGGGCTTTGGGAGACATTCCTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 454 GGGAGCATCGGTTCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 301 GGGAGCATCGGTTCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 514 CACCAAGCGGTGAACACTATCTCCACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 361 CACCAAGCGGTGAACACTATCTCCACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 574 GCGCTGTCATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 421 GCGCTGTCATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 634 AAGGCGGTCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 481 AAGGCGGTCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 694 TTCCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 541 TTCCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 754 TGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 601 TGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 814 TTCAATCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 661 TTCAATCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 874 CTCTATTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 721 CTCTATTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 934 CACATAACCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 781 CACATAACCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 994 TCAAGCCCTCTCTTCCCAATTTCTACAAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 841 TCAAGCCCTCTCTTCCCAATTTCTACAAAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 1054 CAGCCAGGACCTCAAAAACAAAAGGCGGAGAGATGCCAATTTGAACTCGGTGCG
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Db 901 CAGCCAGGACCTCAAAAACAAAAGGCGGAGAGATGCCAATTTGAACTCGGTGCG
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QY 1114 AGGAGTGCATCGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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Db 961 AGGAGTGCATCGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
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QY 1174 CACATTGTTAGTGACACTGA 1194
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Db 1021 CACATTGTTAGTGACACTGA 1041
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RESULT 4
US-09-886-041-1
; Sequence 1, Application US/09886041
; Publication No. US20030059869A1
; GENERAL INFORMATION:
; APPLICANT: XIA, TAI-HE
; APPLICANT: NI, DONGHUI
; APPLICANT: EISHINGREDO, HAIFENG
; APPLICANT: ARDATI, ALI
; APPLICANT: MINNICH, ANNE
; APPLICANT: JUMP, RAY
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR

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: FILE REFERENCE: 41491
: CURRENT APPLICATION NUMBER: US/09/886,041
: CURRENT FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 1041
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-886-041-1

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Query Match	87.1%	Score 1039.4	DB 9	Length 1041
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1040; Conservative	0	Mismatches	1	Indels 0; Gaps 0

Oy	154	ATGTACAAAGGGGTGTCCTCCCGCATGTAGAGGGGGAACACATCTCCAGATGTGCGCG	213
Db	1	ATGTACAAAGGGGTGTCTCTCCGATGTAGAGGGGGAACACATCTCCAGATGTGCGCGG	60
Oy	214	CTGCTCATTTGTGACCTTTTGTGTGTGGGCGCATAGGCAATGGGGGTGGCCTGTGTGTTTC	273
Db	61	CTGCTCATTTGTGACCTTTTGTGTGTGGGCGCATAGGCAATGGGGGTGGCCTGTGTGTTTC	120
Oy	274	TGCTTCCACATGAAGACCTGGAAAGCCAGACACTGTTACTTTTCAATTTGGCCGTGACT	333
Db	121	TGCTTCCACATGAAGACCTGGAAAGCCAGACACTGTTACTTTTCAATTTGGCCGTGACT	180
Oy	334	GATTTCTCTTATGATCTGTGCTGTCTTTTCCGACAGACTATTTACTCAGAGTATGACAC	393
Db	181	GATTTCTCTTATGATCTGTGCTGTCTTTTCCGACAGACTATTTACTCAGAGTATGACAC	240
Oy	394	TGGGCTTTTGGGGACATTTCCCTCCGCGAGTGGGGCTCTTACGTTGGCCATGAACGGGCC	453
Db	241	TGGGCTTTTGGGGACATTTCCCTCCGCGAGTGGGGCTCTTACGTTGGCCATGAACGGGCC	300
Oy	454	GGGAGCATCGTGTTCCTTACGGTGTGGTGGCGGACAGATATTTCAAGTGTCCACCC	513
Db	301	GGGAGCATCGTGTTCCTTACGGTGTGGTGGCGGACAGATATTTCAAGTGTCCACCC	360
Oy	514	CACCAAGGGGTGAACACTATCTCACCCGGGTGGCGGCTGGCATCGTGTGACCCCTGGG	573
Db	361	CACCAAGGGGTGAACACTATCTCACCCGGGTGGCGGCTGGCATCGTGTGACCCCTGGG	420
Oy	574	GGCCTGTCTATCTTGGGAACAGTATCTTTTGTGTGAAACCATCTCTGGGTGCAAG	633
Db	421	GGCCTGTCTATCTTGGGAACAGTATCTTTTGTGTGAAACCATCTCTGGGTGCAAG	480
Oy	634	AGCGCCGTCTCTGTGAGAGGTTTATCATGTGAAGTGGGCCAAATGGCTGGAGACATCATG	693
Db	481	AGCGCCGTCTCTGTGAGAGGTTTATCATGTGAAGTGGGCCAAATGGCTGGAGACATCATG	540
Oy	694	TTCCAGCTGAGATTCTTTATGCCCTCGGATCATCTTATTTTGTCTCTTCAAGATTGT	753
Db	541	TTCCAGCTGAGATTCTTTATGCCCTCGGATCATCTTATTTTGTCTCTTCAAGATTGT	600
Oy	754	TGGAGCTGAGGCGGAGGACACAGCTGGCCGACAGCTTGGATGAAGAAAGCCGACCCG	813
Db	601	TGGAGCTGAGGCGGAGGACACAGCTGGCCGACAGCTTGGATGAAGAAAGCCGACCCG	660
Oy	814	TTTCATCATGTGTGGCAATTGTGTTCATCATCATGCTACTGGCCGACGGTGTCTGTAGA	873
Db	661	TTTCATCATGTGTGGCAATTGTGTTCATCATCATGCTACTGGCCGACGGTGTCTGTAGA	720
Oy	874	CTCTATTTCTTGGAGCGGTGCCTCGATGTCTGTGATCCCTCTGTCTCATGGGGCCCTG	933
Db	721	CTCTATTTCTTGGAGCGGTGCCTCGATGTCTGTGATCCCTCTGTCTCATGGGGCCCTG	780
Oy	934	CACATTAACCTTAGGTTTCACTCATGAACAGATGTGTGATCCCTCGGTGATATATTT	993
Db	781	CACATTAACCTTAGGTTTCACTCATGAACAGATGTGTGATCCCTCGGTGATATATTT	840
Oy	994	TCAGGCCCTCTTTCCAAAATTCTAACAAAGCTCAAAATTCGAGTGTGAACCCCAAG	1053

Accession	Sequence	Length
D8	TCAGGCCCTCTCTTCCAAATTTACACAAAGCTCAAAATCTGACGTGTGAACCCAAAG	900
D8	841 TCAGGCCCTCTCTTCCAAATTTACACAAAGCTCAAAATCTGACGTGTGAACCCAAAG	900
D8	1054 CAGCCAGACACTCAAAAAACACAAAGCCGGAGAGAGATGCCAATTTGCACTCGGTGTC	1113
D8	901 CAGCCAGACACTCAAAAAACACAAAGCCGGAGAGAGATGCCAATTTGCACTCGGTGTC	960
D8	1114 AGAGTTGCATCAGTGTGGCAAAATAGTTTCCAAAGCCAGTGTGATGGGCAATGGGATCCC	1173
D8	961 AGAGTTGCATCAGTGTGGCAAAATAGTTTCCAAAGCCAGTGTGATGGGCAATGGGATCCC	1020
D8	1174 CACATTTGTAGTGGCACTGA	1194
D8	1021 CACATTTGTAGTGGCACTGA	1041

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RESULT 5
US-09-862-274-1
Sequence 1, Application US/09862274
Patent No. US20020052022a1
GENERAL INFORMATION:
APPLICANT: ELSHOUBAGY, NABIL
APPLICANT: GATTU, MAHANANDESHWAR
APPLICANT: SHABON, USMAN
APPLICANT: IGAR, DIANE MICHELE
TITLE OF INVENTION: MOLECULAR CLONING OF A CHEMOKINE LIKE
TITLE OF INVENTION: 77MR (AXOR87)
FILE REFERENCE: GP-70703-1
CURRENT APPLICATION NUMBER: US/09/862,274
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 09/580,675
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: GB 0026639.1
PRIOR FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1041
TYPE: DNA
ORGANISM: HOMO SAPIENS
US-09-862-274-1

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Query Match	87.1%;	Score 1039.4;	DB 10;	Length 1041;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1040;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0;

QY	154	ATGTACAACGGGTGTCGTGTCGCGATGAGAGGGGAGACCAATCTCCAGGAGTATCCGCG	213
Db	1	ATGTACAACGGGTGTCGTGTCGCGATGAGAGGGGAGACCAATCTCCAGGAGTATCCGCG	60
QY	214	CTGCTCATTTGTGGCCCTTGTGCTGGGCGCACTAGGCGAATGGGGTCGGCCGTGTGGTTTC	273
Db	61	CTGCTCATTTGTGGCCCTTGTGCTGGGCGCACTAGGCGAATGGGGTCGGCCGTGTGGTTTC	120
QY	274	TGCTTCACATGAAAGCCTGGAAGCCAGCACTGTTAACTCTTTCAATTTGGCCGGGCT	333
Db	121	TGCTTCACACATGAAAGCCTGGAAGCCAGCACTGTTAACTCTTTCAATTTGGCCGGGCT	180
QY	334	GATTTCCATCCTTAATGATGTGCTGCTTTTGGACAGACATTAACCTCAGACCTAGACAC	393
Db	181	GATTTCCATCCTTAATGATGTGCTGCTTTTGGACAGACATTAACCTCAGACCTAGACAC	240
QY	394	TGGGCTTTTGGGGAATTTCCCTGGCCGAGTGGGGCTCTTCAAGTTGGCCATGAACAGGGCC	453
Db	241	TGGGCTTTTGGGGAATTTCCCTGGCCGAGTGGGGCTCTTCAAGTTGGCCATGAACAGGGCC	300
QY	454	GGGAGCATTCGTCTTCTTAACGTGTGTGCTGCGGACAGGATTTCAAGTGGATCACCCC	513
Db	301	GGGAGCATTCGTCTTCTTAACGTGTGTGCTGCGGACAGGATTTCAAGTGGATCACCCC	360
QY	514	CACCAACGGGTAACACTATCTCAACCCGGGTGCGAGCTGGCATCGTCTGACCCCTGTGG	573
Db	361	CACCAACGGGTAACACTATCTCAACCCGGGTGCGAGCTGGCATCGTCTGACCCCTGTGG	420

QY 574 GCCCTGGTCACTCTGGGAACAGTATCTTTTGTGGAGAACCATCTCTGCGTGAAG 633
 Db 421 GCCCTGGTCACTCTGGGAACAGTATCTTTTGTGGAGAACCATCTCTGCGTGAAG 480
 QY 634 ACCGCGGCTCTCTGGAGAGCTTCATCATGAGTGGCGCAATGGCTGGACAGCATATG 693
 Db 481 ACCGCGGCTCTCTGGAGAGCTTCATCATGAGTGGCGCAATGGCTGGACAGCATATG 540
 QY 694 TTCCAGCTGGAGTCTTTATGCCCCCTCGGCATCATCTTATTTTGGCTCTTCAAGATTGT 753
 Db 541 TTCCAGCTGGAGTCTTTATGCCCCCTCGGCATCATCTTATTTTGGCTCTTCAAGATTGT 600
 QY 754 TGGAGCTGAGGCGGAGGAGGAGAGCTGGCAAGACAGGCTGGATGAGAGAGGAGCCGG 813
 Db 601 TGGAGCTGAGGCGGAGGAGGAGAGCTGGCAAGACAGGCTGGATGAGAGAGGAGCCGG 660
 QY 814 TTCAATCATGAGTGGAGAAATTTGTTCATCATGAGTGGCGCAAGCTGGCGAGCTGTCTGCTAGA 873
 Db 661 TTCAATCATGAGTGGAGAAATTTGTTCATCATGAGTGGCGCAAGCTGGCGAGCTGTCTGCTAGA 720
 QY 874 CTCTATTTCTCTGGAGCGGTGCCCCCTCGAGTGCCTGCGATCCCTGTCCATGGGGCCCTG 933
 Db 721 CTCTATTTCTCTGGAGCGGTGCCCCCTCGAGTGCCTGCGATCCCTGTCCATGGGGCCCTG 780
 QY 934 CACATTAACCTCAAGCTTCACTTACATGAAACAGCATGCTGATCCCTGTGTATTTT 993
 Db 781 CACATTAACCTCAAGCTTCACTTACATGAAACAGCATGCTGATCCCTGTGTATTTT 840
 QY 994 TCAAGCCCTCTCTTCCCAATTTCTACACAGCTCAAAATCTGAGTGGAGAACCCCAAG 1053
 Db 841 TCAAGCCCTCTCTTCCCAATTTCTACACAGCTCAAAATCTGAGTGGAGAACCCCAAG 900
 QY 1054 CAGCGAGACACTCAAAAACACAAAGGCGGAGAGATGCAATTTGCAACTCGGTGCG 1113
 Db 901 CAGCGAGACACTCAAAAACACAAAGGCGGAGAGATGCAATTTGCAACTCGGTGCG 960
 QY 1114 AGAGTTGTCATCTGCTGGCAATAGTTTCCAAAGCCATGCTGATGGGCAATGGATCCC 1173
 Db 961 AGAGTTGTCATCTGCTGGCAATAGTTTCCAAAGCCATGCTGATGGGCAATGGATCCC 1020
 QY 1174 CACATTGTTAGTGGCACTGA 1194
 Db 1021 CACATTGTTAGTGGCACTGA 1041
 RESULT 6
 US-10-094-417-7
 ; Sequence 7, Application US/10094417
 ; Publication No. US20030045685A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tian, Hui
 ; APPLICANT: Zhao, Jilang
 ; APPLICANT: Chen, Jin-Long
 ; APPLICANT: Cutler, Gene
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: No. US20030045685A1e1 Receptors
 ; FILE REFERENCE: 018781-008110US
 ; CURRENT APPLICATION NUMBER: US/10/094,417
 ; CURRENT FILING DATE: 2002-06-10
 ; PRIOR APPLICATION NUMBER: US 09/802,803
 ; PRIOR FILING DATE: 2001-03-09
 ; PRIOR APPLICATION NUMBER: US 60/276,649
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 1041
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR183
 ; NAME/KEY: CDS

; LOCATION: (1)..(1041)
 ; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR183
 US-10-094-417-7
 Query Match 86.8%; Score 1036.2; DB 9; Length 1041;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1038; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 154 ATGTCAACGGGTCGTGCTGGCGCATGAGGGGAGACATCTCCAGGTATGCCCCG 213
 Db 1 ATGTCAACGGGTCGTGCTGGCGCATGAGGGGAGACATCTCCAGGTATGCCCCG 60
 QY 214 CTGCTCATTTGAGCCTTTGTGCTGGGCGCATAGAGCAATGGAGTGGCCCTGTGTTC 273
 Db 61 CTGCTCATTTGAGCCTTTGTGCTGGGCGCATAGAGCAATGGAGTGGCCCTGTGTTC 120
 QY 274 TGCTTCCATGAGAGCCTGGAAGCCGAGCATGTTTTCAATTTGGCCGTGCT 333
 Db 121 TGCTTCCATGAGAGCCTGGAAGCCGAGCATGTTTTCAATTTGGCCGTGCT 180
 QY 334 GATTTCCCTTTATGATGCTGCTGCTTTTGGAGACATTTACCTTCAAGCTAGAC 393
 Db 181 GATTTCCCTTTATGATGCTGCTGCTTTTGGAGACATTTACCTTCAAGCTAGAC 240
 QY 394 TGGGCTTTTGGGGAATTCCTGCGAGTGGGCTTTCAAGTGGCATGAACAGGACC 453
 Db 241 TGGGCTTTTGGGGAATTCCTGCGAGTGGGCTTTCAAGTGGCATGAACAGGACC 300
 QY 454 GGGAGCATGCTGTTCTTTACGCTGCTGGGAGAGATTTTCAAGTGGTCCACCC 513
 Db 301 GGGAGCATGCTGTTCTTTACGCTGCTGGGAGAGATTTTCAAGTGGTCCACCC 360
 QY 514 CACCAAGGAGGAGACATATCTCCACCAGGCTGGGCTGGCATCTGACCTCTG 573
 Db 361 CACCAAGGAGGAGACATATCTCCACCAGGCTGGGCTGGCATCTGACCTCTG 420
 QY 574 GCCCTGATCTCTGGGAACAGTATCTTTTGTGGAGAACCATCTCTGCTGCAAG 633
 Db 421 GCCCTGATCTCTGGGAACAGTATCTTTTGTGGAGAACCATCTCTGCTGCAAG 480
 QY 634 ACGGCGTCTCTGTGAGAGCTTCATGATGAGTGGCCAAATGGCTGGCAAGCATG 693
 Db 481 ACGGCGTCTCTGTGAGAGCTTCATGATGAGTGGCCAAATGGCTGGCAAGCATG 540
 QY 694 TTCCAGCTGAGTCTTTATGCCCCCTGGGATCATCTTATTTGCTCTCCAGATTGT 753
 Db 541 TTCCAGCTGAGTCTTTATGCCCCCTGGGATCATCTTATTTGCTCTCCAGATTGT 600
 QY 754 TGGAGCTGAGGCGGAGGAGCAGCTGGCCAGACAGGCTGGATGAGAGAGGAGCCGG 813
 Db 601 TGGAGCTGAGGCGGAGGAGCAGCTGGCCAGACAGGCTGGATGAGAGAGGAGCCGG 660
 QY 814 TTCAATCATGAGTGGCAATTTGTATTATCATGCTTACTGCTGCCAGGCTGTCTAGA 873
 Db 661 TTCAATCATGAGTGGCAATTTGTATTATCATGCTTACTGCTGCCAGGCTGTCTAGA 720
 QY 874 CTCTATTTCTCTGAGAGGCTGAGGCTGGAGTCCCTGTGCAATGGGGCCCTG 933
 Db 721 CTCTATTTCTCTGAGAGGCTGAGGCTGGAGTCCCTGTGCAATGGGGCCCTG 780
 QY 934 CACATTAACCTCAAGCTTCACTTACATGAAACAGATGCTGATCCCTGTGTATTTT 993
 Db 781 CACATTAACCTCAAGCTTCACTTACATGAAACAGATGCTGATCCCTGTGTATTTT 840
 QY 994 TCAAGCCCTCTCTTCCCAATTTCTACACAGCTCAAAATCTGAGTGGAGAACCCCAAG 1053
 Db 841 TCAAGCCCTCTCTTCCCAATTTCTACACAGCTCAAAATCTGAGTGGAGAACCCCAAG 900
 QY 1054 CAGCGAGACACTCAAAAACACAAAGGCGGAGAGATGCAATTTGCAACTCGGTGCG 1113
 Db 901 CAGCGAGACACTCAAAAACACAAAGGCGGAGAGATGCAATTTGCAACTCGGTGCG 960
 QY 1114 AGAGTTGTCATCTGCTGGCAATAGTTTCCAAAGCCATGCTGATGGGCAATGGATCCC 1173

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Db      961 AGGAGTTCACACACTGTGGGAAAAGTTCGAAAGCAGCTGATGCGAATGGATCC 1020
Oy      1174 CACATTGTTGAGTGCACTGA 1194
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Db      1021 CACATTGTTGAGTGCACTGA 1041

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RESULT 7
US-09-962-832-218

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: Sequence 218: Application US/09962832
: Patent No. US20020110821A1
: GENERAL INFORMATION:
: APPLICANT: Ebner, Reinhard
: TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
: TITLE OF INVENTION: Sets
: FILE REFERENCE: 689290-74
: CURRENT APPLICATION NUMBER: US/09/962,832
: CURRENT FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: US/60/235,077
: PRIOR FILING DATE: 2000-09-25
: PRIOR APPLICATION NUMBER: US/60/235,280
: PRIOR FILING DATE: 2000-09-25
: NUMBER OF SEQ ID NOS: 259
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO: 218
: LENGTH: 2051
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-962-832-218

```

Query Match	30.9%;	Score 369.2;	DB 10;	Length 2051;
Best Local Similarity	64.0%;	Pred. No. 1.5e-109;		
Matches 398;	Conservative	0;	Mismatches 318;	Indels 18; Gaps 2;

Db	637	TTCCCTCCGAGAGTTCCCTCGGCCCTGGGAGATCATCTGTTCTGCTCAGCCAGAAATTATC	696
QY	754	TGAGAGCTTGAGGCGGAGGAGCAGACGCTGGCCAGACAGGCTCGGATGAAGAAAGCCGACCCGG	813
Db	697	TGGAGCCCTGGCGGCGAGG---ACAAATGGAGCCGGCAATGCCAATCAAGAGACCCATACCC	753
QY	814	TTTCATCATGTTGGTGGGGAATTGTGTTTCATCAACATGTCACTCTCCAGCGTGTCTCTAGA	873
Db	754	TTTCATCATGTTGGTGGGGAATTGTGTTTCATCAACATGTCACTCTCTCTCTCCAGCGTGTGTGGGG	813
QY	874	CTCTATTTCCTCTGGACGAGTGCCCTC-----GAGTGGCTTGCAGATCCTCT	918
Db	814	ATTCGGACATCTTCTGGCTCTGGCTCGACACATCTGGGCGAGCAGAAATGTGAAGTGAACGCTGG	873
QY	919	GTCATATGGGGCCCTGCACATTAACCTCTAGTTTACTTAATGAACAGCATGCTGGATCCC	978
Db	874	GTCGACCTGGGGCTTCTTATCACTCTCAGCTTCACTTAATGAACAGCATGCTGGACCCC	933
QY	979	CTGGGTATTAATTTTTCGAAGCCCTCCTTTCCCAATTTCAACAAAGTCAAAATGTGC	1038
Db	934	GTTGGTACTTACTTCTCCAGCCATCTTTCCCAATCTTCTTCTCCACTTGTATCAACGCC	993
QY	1039	AGCTGAAACCCAGCAGCCAGGACACTCAAAA	1072
Db	994	TGCCTCCAGAGAGATGACAGGAGGCCAGATA	1027

```

RESULT 8
US-09-944-807-20
; Sequence 20, Application US/09944807
; Patent No. US20020119494A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082.00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 2051
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-944-807-20

```

Query Match	30.9%;	Score 369.2;	DB 10;	Length 2051;
Best Local Similarity	64.0%;	Pred. No. 1.5e-109;		
Matches 599;	Conservative	0;	Mismatches 318;	Indels 18;
				Gaps 2

QY 454 GGGAGCATGCTGTTCTTACGGTGTGGCTGGAGCAGATATTTCAAAGTGTCCACCCC 513
 DB 397 GGGAGCATGCTGTTCTTACGGTGTGGCTGGAGCAGATATTTCAAAGTGTCCACCCC 456
 QY 514 CACGACGCGGTGAACATATCTCCACCGGTGGCGGTGGCATCTGCTGACCCCTGTGG 573
 DB 457 CACGACGCGGTGAACATATCTCCACCGGTGGCGGTGGCATCTGCTGACCCCTGTGG 516
 QY 574 GCCCTGATCTCTGGAGCAGATGTTATCTTTGTGTGAGAACCATCTCTGCTGCAAGAG 633
 DB 517 GGCATCACTGTGTGGCTTAAAGTCCACCTCTGAAAGAAAGTGTGATCCAGAAATGGC 576
 QY 634 ACGGCGCTCTCTGTGAGACCTTATGATGAGTGGCGCATGCTGGGACGACATCATG 693
 DB 577 CCGTCAATGTGTGATCAGCTTTCAGCATCTGCCATCTTCCGAGTGGGACGAACTATG 636
 QY 694 TTCAGCTGAGTCTTCTTATGAGCCCTGGCATCATCTTATTTGCTTCAAGATTTGT 753
 DB 637 TTCTCTCTGAGTCTTCTCTGCTGCTGCGGACATCTGTTCTGTACGCGAAATTTATC 696
 QY 754 TGAAGCTTGAAGCGGAGGAGCAGACTGGCCAGACAGCTTGTGATGAAGAGCGACCCG 813
 DB 697 TGAAGCTTGAAGCGGAGGAGCAGACTGGCCAGACAGCTTGTGATGAAGAGCGACCCG 753
 QY 814 TTGATCATGTGTGTGAGTGTGTTGTTGATCATGCTTACTGCTCCAGCGTGTCTGTAGA 873
 DB 754 TTGATCATGTGTGTGAGTGTGTTGTTGATCATGCTTACTGCTCCAGCGTGTGTGTGCG 813
 QY 874 CTCTATTTCTCTGAGAGGAGGCTCTC-----GAGTCCCTGGCATCTCTCT 918
 DB 814 ATCCGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 873
 QY 919 GTTCATGAGGCGCTTGCATATACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 978
 DB 874 GTTCATGAGGCGCTTGCATATACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 933
 QY 979 CTGCTGATTTATTTTCAAGCCCTCTTCTTCCAAATTTCTCAACAAGCTCAAAATCTGC 1038
 DB 934 CTGCTGATTTATTTTCAAGCCCTCTTCTTCCAAATTTCTTCTTCTTCTTCTTCTTCTTCT 993
 QY 1039 AGTGTGAACCCAGAGCAGAGCAGACTCAAAA 1072
 DB 994 TGCTTCCAGAGAAATGACAGGTGAGCCAGATA 1027
 RESULT 9
 US-10-092-135-10
 ; Sequence 10, Application US/10092135
 ; Publication No. US20030054374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
 ; FILE REFERENCE: D0134.NP
 ; CURRENT APPLICATION NUMBER: US/10/092,135
 ; PRIOR FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US 60/273,808
 ; PRIOR FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/278,983
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 207
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-10-092-135-10
 Query Match 17.3%; Score 207; DB 9; Length 207;
 Best Local Similarity 100.0%; Pred. No. 2.9e-57;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 205 ATGCCGCGCTGCTCATGTGTGCGCTTTGTGCTGGGCGACTGAGCAATGGGGTGGCCCTG 264

DB 1 ATGCCGCGCTGCTCATGTGTGCGCTTTGTGCTGGGCGACTGAGCAATGGGGTGGCCCTG 60
 QY 265 TGTGCTTCTGCTTCCATATGAAGACCTGGAAGCCAGACACTGTTTCAATTTG 324
 DB 61 TGTGCTTCTGCTTCCATATGAAGACCTGGAAGCCAGACACTGTTTCAATTTG 120
 QY 325 GCCGTGCTGATTTCTCTTATGATGCTGCTGCTTTTGGAGACGATATTTACTGAGA 384
 DB 121 GCCGTGCTGATTTCTCTTATGATGCTGCTGCTTTTGGAGACGATATTTACTGAGA 180
 QY 385 CGTAGACACTGGGCTTTTGGGACATT 411
 DB 181 CGTAGACACTGGGCTTTTGGGACATT 207
 RESULT 10
 US-10-116-252-3
 ; Sequence 3, Application US/10116252
 ; Publication No. US2003028008A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni et al.
 ; TITLE OF INVENTION: Seven Transmembrane Receptor Polynucleotides,
 ; FILE REFERENCE: PTO07P1
 ; CURRENT APPLICATION NUMBER: US/10/116,252
 ; CURRENT FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: US/09/711,909
 ; PRIOR FILING DATE: 2000-11-15
 ; PRIOR APPLICATION NUMBER: PCT/US00/13737
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: 60/135,167
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 60/143,616
 ; PRIOR FILING DATE: 1999-07-13
 ; PRIOR APPLICATION NUMBER: 60/152,934
 ; PRIOR FILING DATE: 1999-09-09
 ; PRIOR APPLICATION NUMBER: 60/189,029
 ; PRIOR FILING DATE: 2000-03-14
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 1423
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-116-252-3
 Query Match 15.9%; Score 190.4; DB 9; Length 1423;
 Best Local Similarity 54.8%; Pred. No. 1.9e-51;
 Matches 446; Conservative 0; Mismatches 356; Indels 12; Gaps 3;
 QY 206 TGCCGCGCTGCTCATGTGTGCGCTTTGTGCTGGGCGACTGAGCAATGGGGTGGCCCTG 265
 DB 9 TGCCGCGCTGCTCATGTGTGTGCTGCTGGGCGACTGAGCAATGGGGTGGCCCTG 68
 QY 266 GTGCTTCTGCTTCCATATGAAGACCTGGAAGCCAGACACTGTTTCAATTTG 325
 DB 69 TCATCTTCTGCTTCCATATGAAGACCTGGAAGCCAGACACTGTTTCAATTTG 128
 QY 326 CCGTGTGATTTCTCTTATGATGCTGCTGCTTTTGGAGACGATATTTACTGAGAC 385
 DB 129 TGGCGCTGATTTCTCTTATGATGCTGCTGCTTTTGGAGACGATATTTACTGAGAC 188
 QY 386 GTAGACACTGGGCTTTTGGGACATTCCCGGAGTGGGCTCTTCAAGTGGCCATGA 445
 DB 189 ATGAGACTGGGCTTTTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 248
 QY 446 ACGAGGCGGAGACATGTTCTTACGAGTGTGCTGGAGACAGATATTTCAAGTGG 505
 DB 249 ACGAGGCGGAGACATGTTCTTCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 308
 QY 506 TCCACCCCGACCAAGCGGTGAACATATCTCCACCGGGTGGGCTGAGATGCTTGA 565

Db 309 TGCAGCCCAACAGCTGCTGAGCCGCTGCTTCCGTGGGGGACAGTGCCTGGGCTGACCGGAG 368
 Qy 566 CCTGTGGGCCCCCTGGTCACTCTGGGAAGAGTGTATCTTTTGTGGAGAAGCACTCTGCG 625
 Db 369 GACTCTGGG---TGGGCAATCTGCTCCTCAACAGGACCTGCTCTGAGCACTTCTCCG 425
 Qy 626 TGCAGAGAGCGGCGCTCTCTGTGAGAGCTTATCATGAGAGTGGCCCAATGCTGGACG 685
 Db 426 GCCCTCTGCTCAGCTACAGAGTGGGACAGAACCCCTCGGCTCGCTCGGCTGGACAC 485
 Qy 686 ACATCATGTTCCAGCTGGAGGTTCTTTATGCCCCCTGGGACATCTTATTTTGTCTCTCA 745
 Db 486 AGGACACTGACTGCTGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
 Qy 746 AGATTGTTGAGCCTGAGCGGAGGACAGCTGAGCAGACAGGCTCGATGAGAGAG 805
 Db 543 TGAAGCATTTGGGCTCAACATCCGGAACCGTGTCTGGGGGGGAGGACGAGCCGAGAGG 602
 Qy 806 CCAACCGGTTCAATCATGTGTGGCAATTTGTTTCAATCATGCTACTGCTGCTGCTGCT 865
 Db 603 CCATGCTGTGCTGAGCAGTGTGGGCGCTGTACACCATCTGCTTCTTGGCCACATCA 662
 Qy 866 CTGCTAGACTATTTTCCCTGAGAGGCTGCTGAGTGCCTGAGTGCCTGCTGCTGCTGCT 925
 Db 663 TCTTTGGCAAGCTTCAATGAGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
 Qy 926 GGGCCCTGACATTA-----CCCTCAGCTTCACTTACATGAAGACATGCTGATGCC 979
 Db 723 GCACACAGCTTCTTCCATGAGCTCCCTGCTTCACTGCTTCACTGCTTCACTGCTTCACT 782
 Qy 980 TGTGTATTATTTTCAAGCCCTCTCTTTCCAA 1013
 Db 783 TGCTTACTGCTTCTCTAGCCCCCACTTCTTCA 816

RESULT 11

US-09-826-508-39
 ; Sequence 39, Application US/09826508
 ; Patent No. US20010025099A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nabil Elshourbagy
 ; APPLICANT: Lisa Vawter
 ; TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
 ; FILE REFERENCE: GP-70744USB
 ; CURRENT APPLICATION NUMBER: US/09/826,508
 ; CURRENT FILING DATE: 2001-04-05
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 39
 ; LENGTH: 1594
 ; TYPE: DNA
 ; ORGANISM: HOMO SAPIENS
 US-09-826-508-39

Query Match 15.9%; Score 190.4; DB 10; Length 1594;

Best Local Similarity 54.8%; Pred. No. 2e-51;
Matches 446; Conservative 0; Mismatches 356; Indels 12; Gaps 3;

Qy 206 TGCCTGGGCGCTGCTATTTGAGCTTTGTGTGGGCGCAGTACAGCAATGGGGTCCCTCT 265
 Db 519 TGGCACCACATCTGGGCTGAGAGTTGTCTGTGGGCTGTGGGGAACAATTGGCCCTCT 578
 Qy 266 GTGGTTTCGCTTCCATGAGACCTGGAAGCCGAGACCTGTTTCACTTTTCAATTGG 325
 Db 579 TCAATTTTCATCACAACGCGGCTGAGACTTCAACAGAGGTTCTGCTGACGCTGG 638
 Qy 326 CCGTGGCTGATTTCTCTTATGATGCTGCTGCTTTTGGACAGACTTATTAAGTCAAG 385
 Db 639 TGGCGGCTGACTTCTCTTATGATGATGCTGCTGCTTCCGCGGAGACTTACTTCTCC 698
 Qy 386 GTAGACACTGGGCTTTTGGGAGATTTCTGCGAGTGGGCTTTCAAGTTGGCCATA 445

Db 699 ATGAGACTGGGCTTTTGGGGCTGCTGCTGCAAGTCAACTCTTCAAGTGTCCACCA 758
 Qy 446 ACAAGGCGGAGACATGCTGTTCTTACGTTGTGGCTGCGACAGATTTTCAAGTGG 505
 Db 759 ACCGACAGGCGAGCTTGTCTTCTTCAAGCCATGCACTCAACCGCTTACGAAAGTGG 818
 Qy 506 TCCACCCCAACACCGGGGAGACATATCTCAACCGGAGTGGGCTGAGTCTGCTCA 565
 Db 819 TGGAGCCCAACACGCTGAGCCGCTGCTGAGGAGCACTGCTGAGGAGTGGGCTGG 878
 Qy 566 CCTGTGGGCCCCCTGATCATCTGAGAAAGTGTATCTTTTGTGAGAAACCATCTGCG 625
 Db 879 GACTCTGGG---TGGGCAATCTGCTTCTCAAGGAGACTGCTCTGAGACCTTCTCG 935
 Qy 626 TGCAGAGAGCGGCTCTCTGTGAGAGCTTATCATGAGTGGCCAAATGCTGGACG 685
 Db 936 GCCCTCTGCTCAGCTACAGGAGTGGGACAGAACCCCTCGGCTCGCTCGCTGGACAC 995
 Qy 686 ACATCATGTTCCAGCTGGAGGTTCTTTATGCCCCCTGGGACATCTTATTTTGTCTCTCA 745
 Db 996 AGGACACTGACTGCTGAGGTTCTTCTGCACTGAGCTGCTGCTGCTGCTGCTGCTGCT 1052
 Qy 746 AGATTGTTGAGCCTGAGCGGAGGACAGCTGAGCAGACAGGCTCGATGAGAGAG 805
 Db 1053 TGAAGCATTTGGGCTCAACATCCGGAACCGTGTCTGGGGGGGAGGACGAGCCGAGAGG 1112
 Qy 806 CCAACCGGTTCAATCATGTGTGGCAATTTGTTTCAATCATGCTACTGCTGCTGCTGCT 865
 Db 1113 CCATGCTGTGCTGAGCAGTGTGGGCGCTGTACACCATCTGCTTCTTGGCCAGATCA 1172
 Qy 866 CTGCTAGACTATTTTCCCTGAGAGGCTGAGTGCCTGAGTGCCTGAGTGCCTGCTGCTGCT 925
 Db 1173 TCTTTGCAATGCTTCAATGAGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
 Qy 926 GGGCCCTGACATTA-----CCCTCAGCTTCACTTACATGAAGACATGCTGATGCC 979
 Db 1233 GCACACAGCTTCTTCCATGAGCTCCCTGCTTCACTGCTTCACTGCTTCACTGCTTCACT 1292
 Qy 980 TGTGTATTATTTTCAAGCCCTCTCTTTCCAA 1013
 Db 1293 TGCTTACTGCTTCTCTAGCCCCCACTTCTTCA 1326

RESULT 12

US-09-962-832-239
 ; Sequence 239, Application US/09962832
 ; Patent No. US20020110821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eberhard Reinhard
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
 ; FILE REFERENCE: 689290-74
 ; CURRENT APPLICATION NUMBER: US/09/962,832
 ; CURRENT FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: US/60/235,077
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: US/60/235,280
 ; PRIOR FILING DATE: 2000-09-25
 ; NUMBER OF SEQ ID NOS: 259
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 239
 ; LENGTH: 2061
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-962-832-239

Query Match 11.4%; Score 136; DB 10; Length 2061;

Best Local Similarity 51.2%; Pred. No. 1.1e-33;
Matches 425; Conservative 0; Mismatches 390; Indels 15; Gaps 4;

Qy 215 TGCTCATTTGAGCTTTGTGCTGGGCGCACTAGCAATGGGCTGCTGTGTGTTCT 274
 Db 557 TGCTGGGCTGAGAGTGTGGCTGCTGCTGGGCAACGCGGTGGAGCTTCC 616

QY 275 GCTTCCATGAAAGCCTGGAAGCCGACACTGTTTACCTTTTCAATTGGCCGTGCTG 334
 Db 617 TGTTCGGGTCAGGGGTGTGGAAGCCGTAACGTGTCTACCTGCTCAACCTGGCCCTGCTG 676
 QY 335 ATTTCCTCTTATGATCTGCTGCTTTTGGACAGATTAATCTCAGAGTAACT 394
 Db 677 ACCGCTGTGGCTGCTGCTGCTGCTTTCTGAGCCGCTTCTACGAGCTCAAGCTT 736
 QY 395 GGGCTTTGGGAGACATTCCTGCGAGTGGGGCTTCAAGTTGGCCATGAAGAGGCGG 454
 Db 737 GGCATCTGGGCGCTGTGGCTGTGCTGGCCCTGGCTTCTGCTGAGACTGAGCCGAGCG 796
 QY 455 GAGCATCTGTTCTTACGAGTGGCTGCGACAGATTTTCAAGTGTCCACCC 514
 Db 797 TGGGATGAGCTTCTGCGCGCGGCTTGGACCGGTAACCTCGGTGTCTCAACCTC 856
 QY 515 ACCACGGGTGAACATATCTCCACCCGGGTGGGGCTGAGTGTCTGACCCCTGTGG 574
 Db 857 GGGCTTAAGTCAACCTGCTGTCTCTCAGCGGCGCTGGGGGCTCGGGGCTGTCTGG 916
 QY 575 CCGTGCATCTGGAAGACGTATCTTGTGAGAAACATCTGTGCTGAGAGA 634
 Db 917 TCTGATGTGCGCTCCTACCTGCGCGCTTGTCTCATCTGTGAGCGCGCCAGAACTCCA 976
 QY 635 CGGCGCTCTCTGAGAGCTTCATCATGAGTCCGCGC-----CAATGGCTGACAGACA 688
 Db 977 CAGAGTCCACATTTCTACTCCAGGCGACAGGCTCTTACAGATCATCTGAGAGAG 1036
 QY 689 TCATGTTCCAGCTGAGTCTTTATGCGCTCGGACATCTTATTTTGTCTCTTCAAGA 748
 Db 1037 CACTCTCTGCTCTTCAAGTTGTCTCTCTCTGCTTGTGCTTCTGCTGAAATGACAGCA 1096
 QY 749 TTGTTTGGAGCCGAGGCGGAGG---CAGAGCTGCGCAGACAGGCTCGATGAAGAAG 805
 Db 1097 TCATCAGGGCTCTCCAGAAAGACTCCGGAGGCTGAGAAACAGCCAACTTCAACGGG 1156
 QY 806 CGACCCGGTTCATCATGAGTGGCAATGTTGTTCATCATCATCTGACCTGCGAGGCTG 865
 Db 1157 CCGAGGACTGCTACCTTGT 1216
 QY 866 CTGCTAGACT-CTATTTCTCTGAGGCTGCGCTCGAGTGTGCTGCTGTCTCAT 924
 Db 1217 TGCCAGAGCTGATGACATCTTCCAGATCTGGGAGCTGAGGCGCTTTGTGAG 1276
 QY 925 GGGGCGCT-----GCACATPACCTCAGCTTCACTTCACTGAACAGAGCTGATCCCC 979
 Db 1277 TGCTCATACCTCGAGTGTACAGGAGGCTCACTTCACTGACAGTGTCTCATACCCCG 1336
 QY 980 TGGTATATATTTTCAAGCCCTCTCTTCCCAATTTCTAACAAGATC 1029
 Db 1337 TGGTATACGCTCTTCTCAAGCCCACTTCAAGAGCTCTTATGAGAGGTC 1386
 RESULT 13
 US-09-954-456-1593
 ; Sequence 1593. Application US/09954456
 ; Patent No. US20020115057A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Paul
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
 ; FILE REFERENCE: 689290-76
 ; CURRENT APPLICATION NUMBER: US/09/954,456
 ; CURRENT FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: US/60/233,617
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: US/60/234,052
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: US/60/234,923
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: US/60/235,134
 ; PRIOR FILING DATE: 2000-09-25

; PRIOR APPLICATION NUMBER: US/60/235,637
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US/60/235,638
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US/60/235,711
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,720
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,840
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,863
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 2276
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 1593
 ; LENGTH: 2061
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-954-456-1593
 Query Match 11.4%; Score 136; DB 10; Length 2061;
 Best Local Similarity 51.2%; Pred. No. 1,1e-33;
 Matches 425; Conservative 0; Mismatches 390; Indels 15; Gaps 4;
 QY 215 TGCTCATTTGAGCCCTTGTGCTGGGCGCACTAGGCAATGGGGTGGCCCTGTGTCTTCT 274
 Db 557 TGTCTGGGCTGAGTGTGGGCTGTGGCTGTGCTGGGCAAGCGGTGGCGCTGTGACCTTCC 616
 QY 275 GCTTCCATGAAAGCCTGGAAGCCGACACTGTTTACCTTTTCAATTGGCCGTGCTG 334
 Db 617 TGTTCGGGTCAGGGGTGTGGAAGCCGTAACGTGTCTACCTGCTCAACCTGGCCCTGCTG 676
 QY 335 ATTTCCTCTTATGATCTGCTGCTTTTGGACAGATTAATCTCAGAGTAACT 394
 Db 677 ACCGCTGTGGCTGCTGCTGCTGCTTTCTGAGCCGCTTCTACGAGCTCAAGCTT 736
 QY 395 GGGCTTTGGGAGACATTCCTGCGAGTGGGGCTTCAAGTTGGCCATGAAGAGGCGG 454
 Db 737 GGCATCTGGGCGCTGTGGGCTGCGGCGCTTGTGCTGCTGCTGAGCTCAAGGCTT 796
 QY 455 GAGCATCTGTTCTTACGAGTGGCTGCGACAGATTTTCAAGTGTCCACCC 514
 Db 797 TGGGATGAGCTTCTGCGCGCGCTTGTGCTCATCTGTGAGCGCTGTCAACCTC 856
 QY 515 ACCACGGGTGAACATATCTCCACCCGGGTGGGGCTGAGTGTCTGACCCCTGTGG 574
 Db 857 GGGCTTAAGTCAACCTGCTGTCTCTCAGGCGGCGCTGAGGCTGTGAGGCGCTGTCTGAG 916
 QY 575 CCGTGCATCTGGAAGACGTATCTTGTGAGAAACATCTGTGCTGAGAGA 634
 Db 917 TCTGATGTGCGCTCCTACCTGCGCGCTTGTCTCATCTGTGAGCGCGCCAGAACTCCA 976
 QY 635 CGGCGCTCTCTGAGAGCTTCATCATGAGTCCGCGC-----CAATGGCTGACAGACA 688
 Db 977 CAGAGTCCACATTTCTACTCCAGGCGACAGGCTCTTACAGATCATCTGAGAGAG 1036
 QY 689 TCATGTTCCAGCTGAGTCTTTATGCGCTCGGACATCTTATTTTGTCTCTTCAAGA 748
 Db 1037 CACTCTCTGCTCTCAAGTTGTCTCTCTTGTGGCTCATCGTGTCTGGAATGACAGCA 1096
 QY 749 TTGTTTGGAGCCGAGGCGGAGG---CAGAGCTGCGCAGACAGGCTCGATGAAGAAG 805
 Db 1097 TCATCAGGGCTCTCCAGAAAGACTCCGGAGGCTGAGAAACAGCCCAAGCTTCAACGGG 1156
 QY 806 CGACCCGGTTCATCATGAGTGGCAATGTTGTTCATCATCATCTGACCTGCGAGGCTG 865
 Db 1157 CCGAGGACTGCTACCTTGT 1216
 QY 866 CTGCTAGACT-CTATTTCTCTGAGGCTGCGCTCGAGTGTGCTGCTGTCTCAT 924
 Db 1217 TGCCAGAGCTGATGACATCTTCCAGAAATCTGGGAGGCTCAAGGCGCTTTGTGAG 1276
 QY 925 GGGGCGCT-----GCACATPACCTCAGCTTCACTTCACTGAACAGAGATGCTGATCCCC 979

Db 1277 TGGCTCATACCTCGCATGTCAAGGCGAGCCCTCACTCACTGACAGTGTCTCAACCCCG 1336
 QY 980 TGGTGTATTATTTTCAAGCCCTCTTTCCCAATTTCAACAAGCTC 1029
 Db 1337 TGGTATACGTCTTCCAGCCCACTTCAGAGCTCTATTCGAGGGGTC 1386

RESULT 14
 US-10-549-1
 ; Sequence 1, Application US/10109549
 ; Patent No. US20020170081A1
 ; GENERAL INFORMATION:

; APPLICANT: Brennan, Thomas J.
 ; APPLICANT: Moore, Mark
 ; APPLICANT: Matthews, William
 ; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING GPR31 GENE
 ; FILE REFERENCE: R-180
 ; CURRENT APPLICATION NUMBER: US/10/109,549
 ; CURRENT FILING DATE: 2002-07-09
 ; PRIOR APPLICATION NUMBER: US 60/280,512
 ; PRIOR FILING DATE: 2001-03-29
 ; PRIOR APPLICATION NUMBER: US 60/326,669
 ; PRIOR FILING DATE: 2001-10-02
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 960
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-109-549-1

Query Match 10.9%; Score 130.6; DB 9; Length 960;
 Best Local Similarity 49.5%; Pred. No. 4; 4e-32;
 Matches 430; Conservative 0; Mismatches 424; Indels 15; Gaps 3;

QY 215 TGGCTATGAGCTTTGCTGGGCGCACTAGGCAATGGGCTCGCCCTGTGTTCT 274
 Db 59 TGTGACACTGAGAGTGTGCTGGCTTATGGCAATCTGTGCTCTGAGACTTCT 118
 QY 275 GCTTCACATGAAGACCTGGAAGCCAGACATGTTTACCTTTTCAATTTGCGGCTG 334
 Db 119 TTACCGCTCAAGATGAGAGCTTTATGCCGTACCTGTTCAACCTGGTGGCTG 178
 QY 335 ATTCTCTCTATGATCTGCTGCTCTTTGCGACAGATTTACTCAGACCTAGACT 394
 Db 179 ACCTGCTATTTGGCCACAGTGGCCATCTTGTGCTCTTATCTGAAGGCAAGACT 238
 QY 395 GGGCTTTTGGGACATTTCCCTGCGGAGTGGGCTTTTCACTTTGCGCATGAAGAGCG 454
 Db 239 GGAACCTTGACACATGCTCTGCACTCTGCTCTTCTTGTGGATTTCACTGTGGT 298
 QY 455 GGAGCATCTGTTCTTACGAGTGGCTGCGGACAGATTTTCAAGTGTCCACCCC 514
 Db 299 TGGAGTAGGCTTCTGATGACAGTGGCTTTAGACCGATCTGATGTGTCAATCTTC 358
 QY 515 ACCAGCGGAGACATATCTCCACCGGGTGGCGGCTGGCAATCGTCTGCACTGTTGG 574
 Db 359 GGGTCAAGATTAAGTCTGCTGTCTGAGGCACTTGGGCACTTCCAGACTCAATTTGGC 418
 QY 575 CCCTGTCATCTGGGAACAGTATCTTTTGTGAGAACATCTTCTGCGTCAAGAGA 634
 Db 419 TTCTGATGTTGTTCACCTCCCAAAACCTTCTCACTTGAAGGACTTACCAAGAAATTC 478
 QY 635 CGG-----CGTCTCTGTGAGAGCTTATCATGAGTGGGCAATGGCTGGACAGACA 688
 Db 479 CGGAATGCCCACTTCTATCCCAAGAGGAGCAAGGCAATGGCACTGCAAGAG 538
 QY 689 TCAATTTCAAGTGTGATTTTATGCGGCGGCAATCTTATTTTGTCTCTTCAAGA 748
 Db 539 TACTTCTTCTTCAAGTCTGCTCTTCTTGGGCTTCACTCTCTCTGCAACAGTGGGC 598

QY 749 TTGTTGAGACCTGAGGCGGAGGC---AGCAGCTGGCCAGACAGGCTCGATGAAGAG 805
 Db 599 TCATCAGACCTCCAGAAAGACTCTCAGAGTCTGACAAACAGCCAGATCCGAGGG 658
 QY 806 CGACCCGTTTCAATGATGTGTGGCAATTTGTATCATCATGCTTACTGCCACAGCT 865
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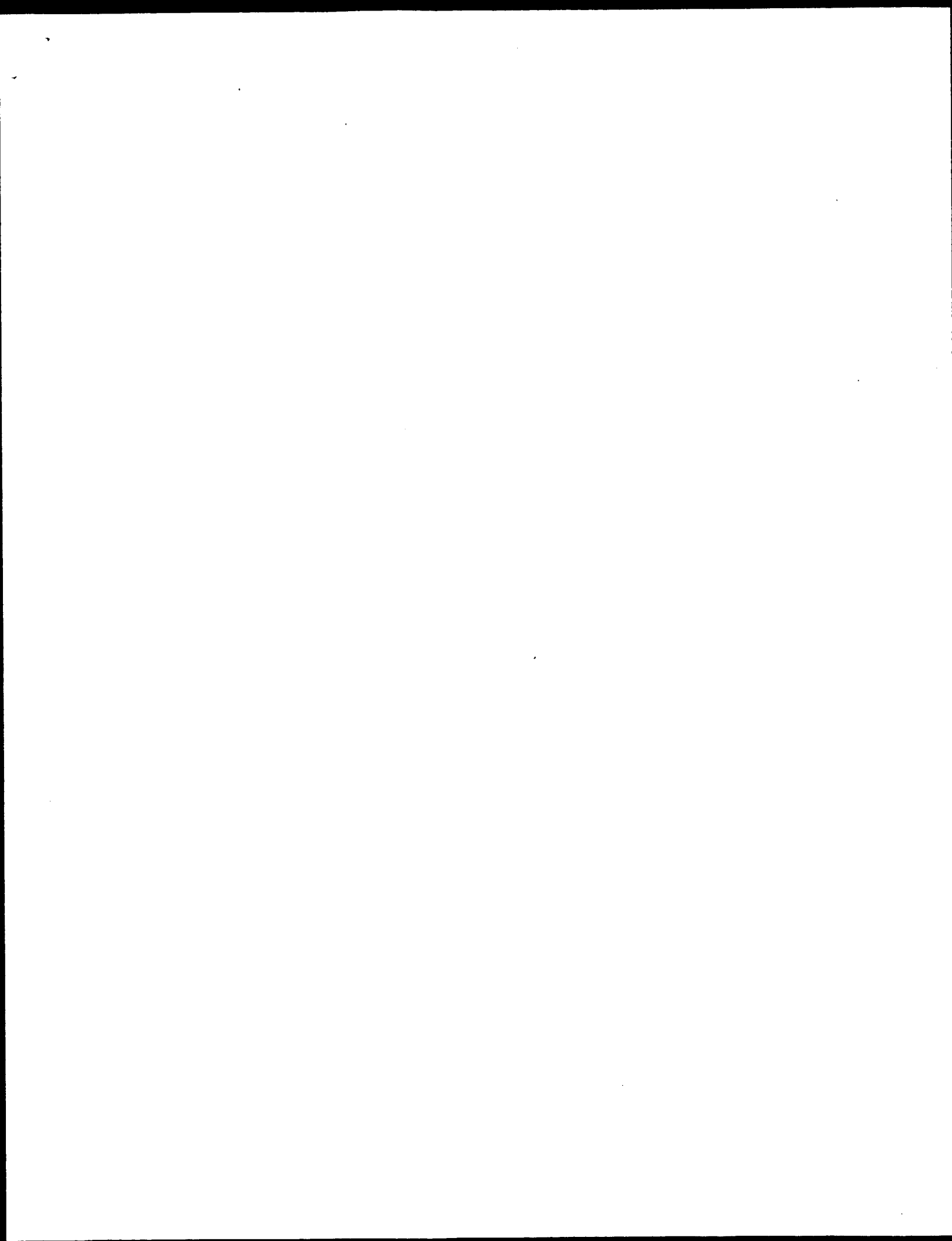
; APPLICANT: GLAXO GROUP LTD
 ; TITLE OF INVENTION: ASSAY
 ; FILE REFERENCE: P79011
 ; CURRENT APPLICATION NUMBER: US/09/788,133
 ; CURRENT FILING DATE: 2001-02-20
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1020
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 US-09-788-133-1

Query Match 9.3%; Score 110.6; DB 10; Length 1020;
 Best Local Similarity 47.2%; Pred. No. 1; 5e-25;
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Search completed: April 3, 2003, 23:57:04
 Job time : 135 secs



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BASE COUNT 289 a 386 c 360 g 337 t

ORIGIN

Query Match 98.7%; Score 1178.4; DB 11; Length 1372;
Best Local Similarity 99.7%; Pred. No. 0;
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RESULT 2
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BC027965
VERSION
BC027965.1 GI:20379752
KEYWORDS
SOURCE
Homo sapiens.
Homo sapiens
ONCANISM

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 2146)
Strausberg, R.
Direct Submision
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nih.gov
Akhter, N., Aylee, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Lark, P., Legaspi, R., Meduro, Q.L.,
Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J.,
Pearson, R., Stenitop, S., Thomas, P.J., Touchman, J.W., Tsurgoun, C.,
Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
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Series: IRAC Plate: 49 Row: 1 Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 5174460

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 DB 509 GGCATCTACTATTTGGCCCTGACAGTCACTCTGAAAGAAAGATCCGATCCAGATGAC 568
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 1 (bases 1 to 885)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr.
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 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact: Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
 Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com"

BASE COUNT 170 a 252 c 229 g 234 t
 ORIGIN
 JOURNAL

Query Match 26.7%; Score 318.8; DB 9; Length 885;
 Best Local Similarity 65.1%; Pred. No. 1.1e-80;
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1057)
 NIH-MGC http://mgc.ncbi.nlm.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation (LNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLNL12774 row: 5 column: 08

High quality sequence stop: 691.

FEATURES

source

Location/Qualifiers

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/lab_host="DH10B"

/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT

211 a 303 c 274 g 269 t

ORIGIN

Query Match

Best Local Similarity 26.0%; Score 310.8; DB 14; Length 1057;

Matches 481; Conservative 0; Mismatches 262; Indels 3; Gaps 1;

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RESULT 6

BI837965

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. NIH-MGC <http://mgs.nci.nih.gov/> Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov> Plate: LLNL1560 row: b column: 01 High quality sequence stop: 796.

FEATURES

source

Location/Qualifiers

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/lab_host="DH10B"

/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT

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ORIGIN

Query Match

Best Local Similarity 26.0%; Score 310.6; DB 13; Length 801;

Matches 466; Conservative 0; Mismatches 239; Indels 2; Gaps 1;

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Qy 634 ACGGCGCTCTCTGAGAGCTTTCATCATGAGTGGCCATGCTGTGACGACATCATG 693
Db 577 GGTGCAAAATTTGAGAGCTTTCATCATGAGTGGCCATGCTGTGACGACAGATG 636
Qy 694 TTCCAGCTGAGATCTTTTATGCCCCCGGATCATCTTATTTGCTCTCAAGATTTT 753
Db 637 TTCTCTCTGAGTCTTCTGCTGCGGCGGATCATCTGTTGCTGAGCCGAATTTATC 696
Qy 754 TGGAGCTGAGCGAGAGAGAGAGAGTGGCCAGAGCTCGATGAGAGAGAGAGAGAG 813
Db 697 TGGAGCTGAGCGAGAGAGAGAGAGTGGCCAGAGCTCGATGAGAGAGAGAGAGAG 754
Qy 814 TTTCATCATGTTGGTGGCAATTTGTTTCATCATCATGCTACCTGCGAG 860
Db 755 TTTCATCATGTTGGTGGCAATTTGTTTCATCATCATGCTACCTGCGAG 801

RESULT 7
BM923028 1076 bp mRNA linear EST 12-MAR-2002
LOCUS BM923028
DEFINITION AGENCOURT 6631998 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5756984
5', mRNA sequence.
ACCESSION BM923028.1 GI:19373407
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1076)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLN at:
http://image.jnl.gov
Place: LMAN12798 row: h column: 09
High quality sequence start: 4
Location/Qualifiers
1..1076
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5756984"

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/clone_11b="NIH_MGC_118"
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/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source: leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC library."
BASE COUNT 211 a 323 c 260 g 281 t 1 others
ORIGIN
Query Match 25.8%; Score 308.6; DB 14; Length 1076;
Best Local Similarity 65.5%; Pred. No. 1e-77;
Matches 468; Conservative 0; Mismatches 244; Indels 3; Gaps 1;
Qy 154 ATGTACAAGGGTGTGCTGTCGCGCATGAGGGGACACCATCTCCAGGTGATGCCCG 213
Db 89 ATGACAGAGAAAGTGTGTGTGTTCCGAGATGACTTATGCAAGGTGTGGCGCG 148
Qy 214 CTGCTATTGTGCTTGTGCTGGGCGCACTAGGCAATGGGGTGGCCCTGTGTGTTTC 273
Db 149 GTGTGGGGCTGAGATTATCTTTGGGCTTGGGCAATGGGCTTGGCTGTGATTTTC 208
Qy 274 TGTTCACATGAAAGACCTGGAAGCCAGACACTGTTTCACTTTTCAATTGGCCGTGCT 333
Db 209 TGTTCACATGAAAGACCTGGAAGATCAACCGGATTTCTGTTCACTGCGAGTAGT 268
Qy 334 GATTTCCTCTTATGATGTGCTGCTCTTTCGAGACACTATTAACCTCAGAGTAGAC 393
Db 269 GACTTCTACTATCATCTGCTGCGCTTGTGATGATGATGATGATGATGATGATGATG 328
Qy 394 TGGGCTTTGGGAGACTTCCCTGCGAGTGGGCTTTCACGTGGCCATGAAAGGGGCC 453
Db 329 TGGAGTTTGGGAGACTTCCCTGCGAGTGGGCTTTCACGTGGCCATGAAAGGGGCC 388
Qy 454 GGGAGCATGCTGTTCTCTTACGAGTGGTGGCTGGCGAGAGTATTTCAAGTGTCCACCC 513
Db 389 GCGAGCATCATCTTCTCTCAAGTGGTGGCTGGCGAGAGTATTTCCGGGTGTCCATCCC 448
Qy 514 CACCAAGCGGTGAACACTTATTCACCCGGGTGGGCTGGCATGTGTGACCCCTGTGG 573
Db 449 CACCAAGCGGTGAACACTTATTCACCCGGGTGGGCTGGCATGTGTGACCCCTGTGG 508
Qy 574 GCGCTGTATCTCTGGAACAGTGTATCTTTGTGAGAACCATCTCGGTGCAAGAG 633
Db 509 GCGATCATCTGTGGCTTAACAGTCCACTCTGTAAGAAAGTGTGTATCCAGAAATGGC 568
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Db 569 CTGCAAAATGTGTGATCAGCTTCAAGATCTGCAATCTCCGGTGGAGAGAGATGAG 628
Qy 694 TTCCAGCTGAGTCTTATGATGCTTGGCGATCATTTATTTGCTCTTCAAGATTTGT 753
Db 629 TTCTCTCTGAGTCTTCTGCTGCGGCGGATCATCTTGTGCTCAACGAATATATC 688
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Qy 814 TTTCATCATGTTGGTGGCAATTTGTTTCATCATCATGCTACCTGCGAGCGTGTCTG 868
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RESULT 8
BM920158 1063 bp mRNA linear EST 12-MAR-2002
LOCUS BM920158
DEFINITION AGENCOURT_6706268 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5750043
5', mRNA sequence.

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ACCESSION BM920158
 VERSION BM920158.1 GI:19370537
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1063)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLNL12780 row: g column: 04
 High quality sequence stop: 647.
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 /lab_host="DH10B"
 /note="Organ: pooled pancreas and spleen; Vector:
 pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of spleen and pancreas from 28 yo
 male. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 1.5 kb, insert size range 1-2.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 025. Note: this is a NIH-MGC Library."
 BASE COUNT 208 a 320 c 259 g 276 t
 ORIGIN

Query Match 25.4%; Score 303; DB 14; Length 1063;
 Best Local Similarity 65.1%; Pred. No. 4.3e-76;
 Matches 463; Conservative 0; Mismatches 245; Indels 3; Gaps 1;

154 ATGTACACAGGGTCTGCTGCCGATCGAGGGGACACCATCTCCAGGTGATGCCGCG 213
 114 ATAGACAAAGAACTGCTGTGTGTTCCGAGATGACTTATGCGCAAGGTGTGCCGCG 173
 214 CTGCTATTGTGCTTGTGCTGGGCGCACTAGGCAATGGGGTCCCTGTGTGTTTC 273
 174 GTGTTGGGGCTGAGTTTATCTTTGGGCTTGGGCAATGGGCTTCCCTGTGATTTTC 233
 274 TGTTCACATGAAGACCTGGAAAGCCAGACAGTTCCTTTCAATTGGCCGCGT 333
 234 TGTTCACATGAAGCTCGGAATCCAGCCGATTTTCTGTTCACCTGGAGAGTCT 293
 334 GATTTCTCTTATGATCTGCTGCTCTTTTGGACAGACTATTAATCTTCAGCTAGAC 393
 294 GACTTTCTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 353
 394 TGGGCTTTTGGGACATTCCTCCGAGTGGGGCTTTTCAAGTTGGCCATGAAGGGCC 453
 354 TGGAGTTTGGGACATTCCTCCGAGTGGGGCTTTTCAAGTTGGCCATGAAGGGCC 413
 454 GGGAGCATGTGTTCTTACGCTGGTGGGCTGGGACAGGATTTTAAATGGTCAAGCC 513
 414 GGGAGCATGTGTTCTTACGCTGGTGGGCTGGGACAGGATTTTAAATGGTCAAGCC 473
 514 CACCAAGCGGTGAACATCTTCCACCGGGTGGCGGCTGGAGTGTGCAACCTGTGG 573
 474 CACCAAGCGGTGAACATCTTCCACCGGGTGGCGGCTGGAGTGTGCAACCTGTGG 533

574 GCCCTGTCATCTCTGGAAACAGTATCTTTTGTCTGAGAAACATCTCTGCGCAAG 633
 534 GGCATCACTGTGGCTTAACAGTCCACCTCTGTAAGAAAGTGTGATCAAAATGCG 593
 634 ACGCGCTCTCTCTGAGAGGCTTATCATGAGTGGGCCAATGGCTGCGACGATCATG 693
 594 CTTGAAATGTGTGATCATGCTTGAAGATCTGCGATACCTTCGGTGGCAAGGCTATG 653
 694 TTCCAGCTGAGTTCCTTATGCTCCCTGGGATCATCTTATTTTGTCTCTTCAAGATTGT 753
 654 TTCTCTCTGAGTTCCT 713
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 814 TTCAATCATGAGTGGGCAATGTGTTTATCATCATGATCACTGCGCCAGCGG 864
 771 TTCAATCATGAGTGGGCAATGTGTTTATCATCATGATCACTGCGCCAGGAG 821

RESULT 9
 LOCUS AL554198 855 bp mRNA linear EST 16-FEB-2001
 DEFINITION AL554198 L1_NFL006_P12 Homo sapiens cDNA clone CS0D1081YK03 5
 prime, mRNA sequence.
 ACCESSION AL554198
 VERSION AL554198.1 GI:12894744
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 855)
 Li, W.B., Gruber, C., Jesse, J. and Polyes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 JOURNAL Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 COMMENT

FEATURES
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 /clone="CS0D1081YK03"
 /clone_1b="L1_NFL006_P12"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact: Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com>"
 BASE COUNT 172 a 240 c 210 g 214 t 19 others
 ORIGIN

Query Match 24.4%; Score 291; DB 9; Length 855;
 Best Local Similarity 61.9%; Pred. No. 1.1e-72;
 Matches 451; Conservative 15; Mismatches 260; Indels 3; Gaps 1;

154 ATAGCAACGGGTCTGCTGCCGATCGAGGGGACACCATCTCCAGGTGATGCCGCG 213
 91 ATAGCAACGGGTCTGCTGCCGATCGAGGGGACACCATCTCCAGGTGATGCCGCG 150
 214 CTGCTATTGTGCTTGTGCTGGGCGCACTAGGCAATGGGGTCCCTGTGTGTTTC 273
 151 GTGTTGGGGCTGAGATTATCTTCCGGCTTCTGGGCAATGGCCTTGCCTGTGGATTTC 210

US-09-942-374-1.rst

Email: cgapds-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LLM1543 row: P column: 17
High quality sequence stop: 731.

Location/Qualifiers
1. .734

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/db xref="taxon:9606"
/clone="IMAGE:5216513"
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/lab_host="DH10B"
/name="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source: leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

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Similarity: 22.8%; Score 272; DB 13; Length 734;
 66.0%; Prof No 3 30 27

409; Conservative 0; Mismatches 210; Indels 1; Gaps 1;

GTTACAAAGCGGGTCTGTCTGCGCATGAGGGGGACACCAATCTCCAGGTGATGCCGCC 213
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 TGCTCATTTGTGGACCTTTGTGCTGGGCGCACTAGGCAATGGGGTGGCCCTGTGTGTTTC 273
 GTTTGGGGCTGGAGTTTATCTTTGGGCTTTGGGCAATGGCCTTGCCCTGTGGATTTC 204
 GCTTCCACATGAAAGACCTGGAAAGCCGAGCACTGTTTAACTTTCAATTTGGCCGTGCT 333
 GTTTCACACTCAAGTCTCGAAATCCAGCCGGAATTTCTGTTCAACCTGGCAGTAGCT 264
 TTTTCCTCTTATGATCTGCTGCTCTTTTGGACAGCTATTTACCTGAGAGTAGAC 393
 CTTTCTACTGATCACTCTGCTGCTGCTTGTGTATGACATCTATGTGCGGGGTTCAGAC 324
 GGGCTTTTGGGACAATCCCTGCGGAGTGGGGCTTTTCAAGTTGGCCATGAAAGGGCC 453
 GAAAGTTTGGGACATCCCTTGGCGGCTGGTGTCTTCAATGTTTGCATGAAC -CGCA 383
 GAGAGCATGTGTCTCTTAGCGTGTGGCTGGCGGAGGTATTTCAAGTGTCCACCCC 513

Db	384	GGCAGCATCATATTCCTCAGCGTGTGGCGGTAGACAGATATTTTCGGGTGTGCATATCC	444
Qy	514	CACCAAGCGGGAACACTATATCTTCACCCGGGTGGCTGGCATGTGTGCACCTGTGG	574
Db	444	CACCAAGCGCTGAACAGATGTCCAAATTGGACACAGCATCATCTCTTGCTTCTGTGG	503
Qy	574	GCCCTGTATCTCTGGGAACAGTATCTTTTGTGTGGAAACCATCTCTGGTGCAGAG	633
Db	504	GGCATCATGTGTGGCGCTTAACAGTCAACTCTTGAAGAAAGATTGTGATTCANAAATGGC	563
Qy	634	ACGGCGCTCTCCTGGAGAGCTCATATGAGATGGCCATGGCTGGCACACATATATG	693
Db	564	ACTGCAATGTGTGATAGCTTCAAGCATCTGCCATACCTTCCGATGACAGAACTATG	623
Qy	694	TTCCAGCTGAGATTCTTTATGCCCTCGGCATCATCTTATTTTGCTCCTTCAGATTGT	753
Db	624	TTCTCTCTGGAGATCTTCTCCTCCCTGGCATCATCTGTCTCTCAGCAGAAATTATC	683
Qy	754	TGAGCTGAGCGAGGCA	773
Db	684	TGGAGCTTGGCGGACAGACA	703

RESULT	12
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LOCUS	752 bp mRNA linear EST 30-Oct-2001
DEFINITION	G09318002F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450832 5' ,
ACCESSION	BM008116
VERSION	BM008116.1 GI:16522470
KEYWORDS	EST.
SOURCE	human.

ORGANISM	REFERENCE	AUTHORS	JOURNAL	COMMENT
Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
1 (bases 1 to 752)				
NIH-MGC http://mgc.nci.nih.gov/ .				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph. D.				

Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>
Plate: LLCMI940 row: d column: 01
High quality sequence scrop: 752.

FEATURES	Location/Qualifiers
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/db xref="taxon:9606"
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/lab host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NH_MGC Library."
BASE COUNT      153 a      216 c      193 g      190 t
ORIGIN

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Query Match:	22.5%	Score 268.8	DB 13	Length 755
Best Local Similarity	65.6%	Prod. No. 2.8e-66		
Matches 407; Conservative	0	Mismatches 212;	Indels 1;	Gaps 1;
154	ATGTACACGGGTCTGCTGCGCATCGAGGGGACACCATCTCCAGGTGATGCCGCG	213		

Db 130 ATAGACAAAGAAAGCTGCTGTGTGTTCCGAGATGACTTATGTCAGGTGTGCGCCG 189
 Qy 214 CTGCTCATTTGGCCCTTGTGCTGGCGCACTAGGCAATGGGCGCCCTGTGTGTTTC 273
 Db 190 GGTGTGGGGCTGAGTTTATCTTGGGGCTTCTGGGGAATGGGCTTGGCCCTGGAGATTTTC 249
 Qy 274 TGTGTCACATGAAAGCCGGAAGCCAGACAGTGTACCTTTCAATTTGGCCGTGCT 333
 Db 250 TGTTCACACTCAAGTCTGGAATTCACCGGATTTTCTGTTCACTGGCAATGCT 309
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 Db 310 GACTTCTATGATGATGATGCTGCTGCTTCTGATGACACATATGTAGGCGTGGAGC 369
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 Db 370 TGGAGATTTGGGAGCAATCTCCCTGCGAGTGGGCTTTTACATGTGGCTAAGAGCGCAG 429
 Qy 454 GGGAGATGCTGTTTCTTACGAGTGGGCTGCGAGCAGAGTATTTCAAGTGGTCAACCC 513
 Db 430 GGGAGATGCTTCTTCTTACGAGTGGGCTGCGAGCAGAGTATTTCCGGTGGTCAATCC 489
 Qy 514 CACCAAGCGGTGAACACTATCTTCCACCCGAGTGGCGCTGGCATGCTGACCCCTGTGG 573
 Db 490 CACCAAGCGGTGAACACTATCTTCCACCCGAGTGGCGCTGGCATGCTTGGCTGTGG 549
 Qy 574 GCGCTGATCTCTGGGAGACAGTGTATCTTTCTGAGAGACATCTTGGCTGCAAGAG 633
 Db 550 GGCATCACTATTGGCGCTGAGTCCACCTTCCGTAAGAGAA-GATGCCATCCAGAAATGG 608
 Qy 634 AGGCGGTCTCTGAGAGCTTCAATGAGAGTGGCGCAATGGCTGGAGCAATCATG 693
 Db 609 CGGTCAATTTGTCAGAGCTTCAAGCATGTCATACCTTCAGTGGAGCAAGCATG 668
 Qy 694 TTCAGCTGAGATCTTATGACCCCTGGGATCATCTTATTTGCTTCAAGATTGTT 753
 Db 669 TTCCTCTGAGATCTTCTTCTGAGTGGGCTGGGATCATCTTACTGCTGACGAGAAATTATC 728
 Qy 754 TGGAGCTTGGGAGGAGGCA 773
 Db 729 TGGAGCTTGGGAGGAGGCA 748

RESULT 13
 BB873518 367 bp mRNA linear EST 27-NOV-2001
 LOCUS BB873518 RIKEN full-length enriched, 15 days embryo brain Mus
 DEFINITION musculus cDNA clone G630046N17.5', mRNA sequence.
 ACCESSION BB873518
 VERSION BB873518.1 GI:17119728
 KEYWORDS EST.
 SOURCE mouse.
 ORGANISM Mus musculus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 367)
 Akimura, T., Arikawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
 Hayatsu, N., Hirakawa, K., Hiraoka, T., Hirozane, T., Imochi, K., Ishi,
 Y., Ito, M., Kawai, J., Kojima, Y., Kondo, M., Matsuyama, T.,
 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
 Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
 Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa,
 A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toyo, T.,
 Watanabe, A., Yasunishi, A., Yamamoto, M., Muramatsu, M., and Hayashizaki, Y.
 RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
 2001)

JOURNAL
 COMMENT
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsukuba, Ibaraki, Japan

Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh,
 M., Kondo, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura,
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
 Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multichipillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kondo, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
 Y., and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES

source
 Location/Qualifiers
 1. 367
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="G630046N17"
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 day_stage=16 days neonate, sex=mixed)
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 sex=male), (tissue_type=whole body, dev_stage=9 days
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 Best Local Similarity 82.5%; Pred. No. 1.2e-63;
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 Db 8 CTCCTCAACTGCTATGAGCAACGGGTGTGCTGCTCATGAGGGGAGGCCATCTCCCA 67
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 Qy 261 CCGTGTGCTTCTGCTTCAATGAAGACCTGGAAGCCAGCACTGTTTACCTTTTCAA 320
 Db 128 CCGTGTGCGCTTCTGCTTCAATGAAGACCTGGAAGCCAGCACTGTTTACCTTTTCAA 187
 Qy 321 TTGGCGCGGTGATTTCTCTTATGATGCTGCTGCTTTCGCAACAATTTTACCT 380
 Db 188 CTTGGCTGTGCGCATTTTCTCCATGATCTGCTTACCCCTTCCGCAACAATTTTACCT 247
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 Db 248 CAGAGTGAACAGTGGGCTTTGGGAGCATCTCCCTGCGAGTGGGCTCTTCAAGTGGC 307
 Qy 441 CATGAACAGGCGCGGAGCATGTTCTTCAAGTGGTGGCTGGAGAGGATTTTCAA 500
 Db 308 CATGAATGAGGCGCGGAGCATTTCTTCTTCAAGTGGTGGCTGGAGAGGATTTTCAA 367

